

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald
- (ii) TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
- (iii) NUMBER OF SEQUENCES: 355
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SEED and BERRY LLP
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: USA
(F) ZIP: 98104-7092
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 05-MAY-1998
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Maki, David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 210121.411C9
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (206) 622-4900
(B) TELEFAX: (206) 682-6031
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 766 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

10081843.022502

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGGCACCG	GTAGTTTGAA	CCAAACGCAC	AATCGACGGG	CAAACGAACG	GAAGAACACA	60
ACCATGAAGA	TGGTGAATC	GATCGCGCA	GGTCTGACCG	CCGCGGCTGC	AATCGGCGCC	120
GCTGCGGCCG	GTGTGACTTC	GATCATGGCT	GGCGGCCCGG	TCGTATACCA	GATCGACGCC	180
GTGCTCTTCG	GCGCGCCACT	GCGGTTGGAC	CCGCGATCCG	CCCCTGACGT	CCCGACCGCC	240
GCCCAGTTGA	CCAGCCTGCT	CAACAGCCTC	GCCGATCCCA	ACGTGTCTGT	TGCGAACAAAG	300
GGCAGTCTGG	TCGAGGGCGG	CATCGGGGGC	ACCGAGGCGC	GCATCGCCGA	CCACAAGCTG	360
AAGAAGGCCG	CCGAGCACGG	GGATCTGCCG	CTGTCTGTTC	CGGTGAAGAA	CATCCAGCCG	420
GCGGCCGCCG	GTTCGGCCAC	CGCCGACGTT	TCCGTCTCGG	GTCCGAAGCT	CTCGTCGCCG	480
GTCAACGAGA	ACGTCACGTT	CGTGAATCAA	GGCGGCTGGA	TGCTGTTCAG	CGCATCGGCG	540
ATGGAGTTGC	TGCAGGCGCG	AGGGAACACT	ATTGGCGGGC	CGGNTTCAGC	CCGCTGTCCA	600
GCTACGCCCG	CCGCCCTGGT	ACGCGTCCAT	GTGGAACACT	CGCGCGTGTA	GCACGGGTGCG	660
GTNTGCGCAG	GGNCGCACGC	ACCGCCCGGT	GCAAGCCGTC	CTCGAGATAG	GTGGTGNCTC	720
GNACCAGNG	ANCAACCCCN	NNTCGNCTNT	TCTCGNTGNT	GNATGA		766

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCATCACC	ATCACCATCA	CGATGAAGTC	ACGGTAGAGA	CGACCTCCGT	CTTCCGCGCA	60
GACTTCTCTA	GCGAGCTGGA	CGTCTCTCG	CAAGCGGGTA	CGGAGAGCCG	GGTCTCCGGG	120
GTGGAAGGGC	TCCCGCCGGG	CTCGGCGTTG	CTGGTAGTCA	AACGAGGCCG	CAACGCCGGG	180
TCCCGGTTCC	TACTCGACCA	AGCCATCACG	TCGGCTGGTC	GGCATCCCGA	CAGCGACATA	240
TTTCTCGACG	ACGTGACCGT	GAGCCGTCG	CATGCTGAAT	TCCGGTTGGA	AAACAACGAA	300
TTCAATGTGC	TCGATGTCGG	GAGTCTCAAC	GGCACCTACG	TCAACCGCGA	GCCCGTGGAT	360
TCGGCGGTGC	TGGCGAACGG	CGACGAGGTC	CAGATCGGCA	AGCTCCGGTT	GCGTCTCTTG	420
ACCGGACCCA	AGCAAGCGCA	GGATGACGGG	AGTACCGGGG	GCCCGTGAGC	GCACCCGATA	480
GCCCCGCGCT	GGCCGGGATG	TCGATCGGGG	CGGTCTCTCG	ACCTGCTACG	ACCGGATTTT	540
CCCTGATGTC	CACCATCTCC	AAGATTCGAT	TCTTGGGAGG	CTTGAGGGTC	NGGGTGACCC	600
CCCCGCGGGC	CTCATTCCNG	GGTNTCGGCN	GGTTTCACCC	CNTACCNACT	GCCNCCCGGN	660
TTGCNAATTC	NTTCTTCNCT	GCCCNNAAG	GGACNNTTAN	CTTGCGCGTN	GAAANGGTNA	720
TCNNGGGCCC	NTCCNTGAAN	CCCNCTCCCC	CT			752

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCATC	ACCATCACCA	TCACACTTCT	AACCGCCAG	CGCGTCGGGG	GCGTCGAGCA	60
CCACGCGACA	CCGGGCGCGA	TCGATCTGCT	AGCTTGAGTC	TGGTCAGGCA	TCGTCGTCAG	120
CAGCGCGATG	CCCTATGTTT	GTGTCGACT	CAGATATCGC	GGCAATCCAA	TCTCCCGCCT	180

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GCGGCGCGCG	GTGCTGCAAA	CTACTCCCGG	AGGAATTTCG	ACGTGCGCAT	CAAGATCTTC	240
ATGCTGTGTA	CGGCTGTGCT	TTTGCTCTGT	TGTTTCGGGTG	TGGCCACGGC	CGCGCCCAAG	300
ACCTACTGCG	AGGAGTTGAA	AGGCACCGAT	ACCGGCCAGG	CGTGCCAGAT	TCAAATGTCC	360
GACCCGGCT	ACAACATCAA	CATCAGCCTG	CCCAGTTACT	ACCCCGACCA	GAAATCGTCC	420
GAAAATTACA	TCGCCAGAGC	GCGCGACAAG	TTCTCAGCG	CGGCCACATC	GTCCACTCCA	480
CGCGAAGCCC	CCTACGAATT	GAATATCACC	TCCGCCACAT	ACCAATCCGC	GATACCGCGC	540
CGTGGTACGC	AGGCCGTGGT	GCTCAMGGTC	TACCACAACG	CCGCGCGCAC	GCACCCAAAG	600
ACCACGTACA	AGGCCTTCGA	TGGGACCAG	GCCTATCGCA	AGCCAATCAC	CTATGACAAC	660
CTGTGCGCAG	CTGACACCGA	TCCGCTGCCA	GTCGTCTTCC	CCATTGTTGC	AAGGTGAAGT	720
GAGCAACGCA	GACCGGGACA	ACWGGTATCG	ATAGCCGCCN	AATGCCCGCT	TGGAACCCNG	780
TGAAATTATC	ACAACCTCGC	AGTCACNAAA	NAA			813

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATGAAC	ACGCCCGCGT	CCGATAACTT	CCAGCTGTCC	CAGGTTGGGC	AGGGATTCCG	60
CATTCCGATC	GGGCAGGCGA	TGGCGATCGC	GGGCCAGATC	CGATCGGGTG	GGGGGTCAAC	120
CACCGTTTCA	ATCGGGCCCTA	CCGCCTTCTC	CGGCTTGGGT	GTTGTCGACA	ACAACGGCAA	180
GGGCGCACGA	GTCCAACGGG	TGGTCGGGAG	CGCTCCGGCG	GCAAGTCTCG	GCAATCCAC	240
CGGCGACGTG	ATCACCGCGG	TGCACGGCGC	TCCGATCAAC	TCCGCCACCG	CGATGGCGGA	300
CGCGCTTAAC	GGGCATCATC	CCGTGACGCT	CATCTCGGTG	AACCTGGCAA	CCAAGTCGGG	360
CGGCACGCGT	ACAGGGAACG	TGACATTGGC	CGAGGGACCC	CCGGCTTGAT	TTCGTCGYGG	420
ATACCACCGT	CCGCGCGGCC	AATTGGA				447

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCCACTGC	GGTCGCGGAG	TATGTCGCCC	AGCAAAATGTC	TGGCAGCCGC	CCAACGGAAT	60
CCGGTGATCC	GACGTGCGAG	GTGTCGAAC	CCGCCGCCGC	GGAAGTATCG	GTCCATGCGT	120
AGCCCGGCGA	CGCGAGCGC	CGGAATGBCG	CGAGTGAGGA	GGCGGGCAAT	TTGGCGGGGC	180
CCGCGCAGCG	NGAGCGCCCG	AATGGCGCGA	GTGAGGAGGT	GGNCAGTCAAT	GCCCCAGNTG	240
ATCCAATCAA	CCTGNATTGC	GNCTGNGGGN	CCATTTGACA	ATCGAGGTAG	TGAGCGCAAA	300
TGAATGATGG	AAAACGGGNG	GNGACGTCCG	NTGTTCTGGT	GGTGNTAGGT	GNCTGNCTGG	360
NGTNGNGGNT	ATCAGGATGT	TCTTCGNCGA	AANCTGATGN	CGAGGAACAG	GGTGNTCCCG	420
NNANNCCNAN	GGNGTCCNAN	CCCNNNNTCC	TCGNCGANAT	CANANAGNCG	NTTGATNGGA	480
NAAAAGGGTG	GANCAGNNNN	AANTNGNGGN	CCNAANAANC	NNANNGNNGN	NNAGNTNGNT	540
NNNTNTTNNC	NNNNNNNTG	NNGNNGNNCN	NNNCAANNNN	NTNNNNNGAA	NNGGNTTNTT	600
NAAAT						604

(2) INFORMATION FOR SEQ ID NO:6:

10084843.022502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGCANGTCG	AACCACTCA	CTAAAGGGAA	CAAAGCTNG	AGCTCCACCG	CGGTGGCGGC	60
CGCTCTAGAA	CTAGTGKATM	YYYCKGGCTG	CAGSAATYCG	GYACGAGCAT	TAGGACAGTC	120
TAACGGTCCT	GTTACGGTGA	TCGAATGACC	GACGACATCC	TGCTGATCGA	CACCGACGAA	180
CGGGTGCAG	CCCTCACCT	CAACCGGCG	CAGTCCCGYA	ACGCGCTCTC	GGCGGCGCTA	240
CGGGATCGGT	TTTTCGCGGY	GTTGGYCGAC	GCCGAGGYCG	ACGACGACAT	CGACGTGCTC	300
ATCTCACCG	GYGCGGATCC	GGTGTCTG	GCCGAGCTGG	ACCTCAAGGT	AGCTGGCGCG	360
GCAGACCGCG	CTGCCGGA	TCTACCGCG	GTGGGCGGCC	ATGACCAAGC	CGGTGATCGG	420
CGCGATCAAC	GGCGCGCGG	TCACCGCGG	GCTCGAAGT	GGCGTGTACT	GCGACATCTT	480
GATCGCTTCC	GAGCAGCGCC	GCTTCGNCGA	CACCCACGCG	CGGGTGGGGC	TGCTGCCAC	540
CTGGGGACTC	AGTGTGTGCT	TGCCGCAAAA	GGTCGCATC	GGNCTGGGCC	GGTGATGAG	600
CTGACCGGC	GACTACCTGT	CGTGACCGA	CGC			633

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACGACGAC	GGCGCGGAG	AGCGGGCGCG	AACGGCGATC	GACGCGGCC	TGGCCAGAGT	60
CGGCACCAAC	CAGGAGGGAG	TCGAATCATG	AAATTGTCA	ACCATATTGA	GCCCGCTCGG	120
CCCCCGCGAG	CCGCGCGCG	GGTCGCGGAG	GTCTATGCCG	AGGCCCGCGC	CGAGTTCGGC	180
CGGCTGCGCG	AGCCGCTCGC	CATGCTGTCC	CCGGACGAGG	GACTGCTCAC	CGCCGGCTGG	240
GCGACGTTGC	GCGAGACACT	GCTGGTGGG	CAGGTGCCGC	GTGGCCGCAA	GGAGCCGCTC	300
GCGCCCGCG	TCGCGGCCAG	CCTGCGCTGC	CCCTGGTGGC	TCGACGCACA	CACCACCATG	360
CTGTACCGCG	CAGGCCAAAC	CGACACCGCC	GCGGCGATCT	TGGCCGGCAC	AGCACTTGCC	420
CGCGGTGACC	CGAACCGGCC	GTATGTGGCG	TGGGCGGCAG	GAACCGGGAC	ACCGCGGGGA	480
CGCCCGGCAC	CGTTCCGCCC	GGATGTCGCC	GCCGAATACC	TGGGCACCGC	GGTGCAATTC	540
CACCTTCATG	CACGCCCTGG	CCTGGTCTG	CTGGACGAAA	CCTTCTGCC	GGGGGGCCCG	600
CGCGCCCAAC	AGCTCATGCG	CGCGCCCGGT	GGACTGGTGT	TCGCCCGCAA	GGTGCGCGCG	660
GAGCATCGGC	CGGCGCGCTC	CACCCGCCCG	CTCGAGCCGC	GAACGCTGCC	CGACGATCTG	720
GCATGGGCAA	CACCGTCCGA	GCCCATAGCA	ACCGCGTTGC	CCGCGCTCAG	CCACCACTGC	780
GACACCGCG	CGCACCTGCG	GCCACCGACT	CGTCAAGTGG	TCAGGCGGGT	CGTGGGGTGC	840
TGGCACGGCG	AGCCAAATGCC	GATGAGCAGT	CGCTGGACGA	ACGAGCACAC	CGCCGAGCTG	900
CCCGCGGACC	TGCACGCGCC	GCCCGTCTT	GCCTGCTGA	CGCGCTTGGC	CCCGCATCAG	960
GTGACCGAGC	ACGACGTCGC	CGCGGCCCGA	TCCTGCTCG	ACACCGATGC	GGCGCTGGTT	1020
GGCGCCCTGG	CCTGGGCGCG	CTTCACCGCC	GCGCGCGCA	TCGGCACCTG	GATCGGGCGC	1080
GCCGCGGAGG	GCCAGGTGTC	CGCGCAAAAC	CGGACTGGGT	GAGTGTGCGC	GCCCTGTCCG	1140
TAGGGTGTCA	TGCTGCGCCC	GAGGGATCTC	GCGGCGCGCA	ACGAGGTGG	CGACACAGGT	1200
GGAAGCTGCG	CCCACTGGCT	TGCGCCCCAA	CGCCGTCGTG	GGCGTTCCGT	TGGCGCGACT	1260
GGCCGATCAG	GTGCGGCGCG	GCCCTTGGCC	GAAGGTCCAG	CTCAACGTGC	CGTACCGGAA	1320
GGACCGGAGC	GTCACGGGG	GTCACCTGC	GCGCCCAAGG	AA		1362

(2) INFORMATION FOR SEQ ID NO:8:

1084943.022502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCAGCAGCCC CGATATGCCG GGCACCGTAG CGAAAGCCGT CGCCGAGCGA CTCGGGCGCG 60
 GTATCGCTCC CGTTGAGGAC ATTCAGGACT GCGTGGAGGC CCGGCTGGGG GAAGCCGGTC 120
 TGGATGACGT GGCCCCGTGT TACATCATCT ACCGCGAGCG GCGCGCCGAG CTGCGGACGG 180
 CTAAGGCCTT GCTCGGCGTG CGGACGAGT TAAAGCTGAG CTTGCGCGCC GTGACGGTAC 240
 TGCAGGAGCG CTATCTGCTG CACGACGAGC AGGGCCGGCC GGGCCGAGTC ACCGGCGAGC 300
 TGATGGACCG ATCGGCGCCG TGTGTGCGGG CGGCCGAGGA CCAGTATGAG CCGGGCTCGT 360
 CGAGGCGGGT GGGCCGAGCG TTGCGCCAGC TATTACGCAA CCTGGAATTC CTGCGCAATT 420
 CGCCACGCTT GATGAAGTCT GGCACCGACC TGGGACTGCT CGCCGGCTGT TTTGTTCTGC 480
 CGATTGAGGA TTCGCTGCAA TCATCTTTTG CGACGCTGGG ACAGGCCGCC GAGCTGCAGC 540
 GGGCTGAGAG CGGCACCGGA TATGCGTTCA GCCACCTGCG ACCCGCCGGG GATCGGGTGG 600
 CCTCCACGGG CGGCACGGCC AGCGGACCGG TGTGTTTCT ACGGCTGTAT GACAGTCCCG 660
 CGGGTGTGGT CTCATGGGCG GGTGCGCGCG GTGGCGCCTG TATGCTGTG CTTGATGTGT 720
 CGCACCCCGA TATCTGTGAT TTCGTCACCG CCAAGGCCGA ATCCCCCAGC GAGCTCCCGC 780
 ATTTACACCT ATCGGTTGAT GTGACCGAGC CGTTCCTGGG GGCCGTCGAA CGCAACGGCC 840
 TACACCGGCT GGTCATCCCG CGAACCAGCA AGATCGTCGC GCGGATGCCC GCCCGCGAGC 900
 TGTTGACAGC CATCTGCAAA GCCGCGCAGC CCGGTGGGGA TCCTGGGCTG GTGTTTCTCG 960
 ACACGATCAA TAGGGCAAA CCGGTGCCGG GGAGAGGCCG CATCGAGGCG ACCAACCCGT 1020
 CGCGGGAGGT CCCACTGCTG CCTTACGAGT CATGTAATCT CGGCTCGATC AACCTCGCCC 1080
 GGATGCTCGC CGACGGTTCG GTGACTGGG ACCGGCTCGA GGAGGTGCGC GGTGTGCGCG 1140
 TGCGGTTCTT TGATGACGTC ATCGATGTCA GCGCTACCC CTTCGCCGAA CTGGGTGAGG 1200
 CGGCCCGCGC CACCCGCAAG ATCGGGCTGG GAGTCATGGG TTTGGCGGAA CTGCTTCCCG 1260
 CACTGGGTAT TCCGTACGAC AGTGAAGAAG CCGTGCGGTT AGCCACCCGG CTCATCGCTC 1320
 GCATACAGCA GGCGGCGCAC ACGGCATCGC GGAGGCTGGC CGAAGAGCGG GCGGCATTC 1380
 CGCGTTTCAC CGATAGCCGG TTGCGCGGGT CGGGCCCGAG GCGCAACGCA CAGGTACCT 1440
 CCGTCGCTCC GACGGGCA

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGGTGTAAAT CGTGCTGGAT CTGGAACCGC GTGGCCCGCT ACCTACCGAG ATCTACTGGC 60
 GGCGCAGGGG GCTGGCCCTG GGCATCGCGG TCGTCTGAGT CGGGATCGCG GTGGCCATCG 120
 TCATCGCCCTT CGTCGACGAG AGCGCCGGTG CCAAAACCGT CAGCGCCGAG AAGCCGGCCT 180
 CGGCCAGAG CCATCCGGGG TCGCCGGCAC CCAAGCAC CCAGCCGCC GGCGAAACCG 240
 AAGGTAACGC CGCGCGGGCC CCGCCGAGG GCCAAACCC CGAGACACCC ACGCCACCG 300
 CGCGGCTGCA GCGCCGCGCG GTGCTCAAGG AAGGGGACGA TTGCCCGAT TCAGCGCTGG 360
 CGCTCAAGG TTTGACCAAG GCGCCGAGT ACTAGCTCG CGACACCGCG AAGTTACCA 420
 TGGTGGTAC CAACATCGC CTGGTGTCT GTAAACGCGA CGTTGGGGCG GCGGTGTTGG 480
 CCGCTACGT TTAATCGCTG GACAACAAGC GGTGTGTGTC CAACCTGGAC TGCAGCCCT 540
 CGAATGAGAC GCTGGTCAAG ACGTTTTCCC CCGGTGAGCA GGTAACGACC GCGGTGACT 600

GGACCGGGAT	GGGATCGGCG	CGCGCTGCC	CATTGCCGCG	GCCGGGATC	GGCGCGGGCA	660
CCTACAATCT	CGTGGTACAA	CTGGGCAATC	TGCGCTCGCT	GCCGGTCCCG	TTCATCCTGA	720
ATCAGCGCGC	GCCGCGCGCC	GGGCGGGTAC	CCGCTCCGGG	TCCAGCGCAG	GCGCTCCGCG	780
CGGAGTCTCC	CGCGCAAGGC	GGATAATTAT	TGATCGCTGA	TGGTCGATTG	CGCCAGCTGT	840
GACAACCCCT	CGCCTCGTGC	CG				862

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATCAGCA	CGGCAAGGC	GTACATGCC	TCCCTGGGTG	TGCAGGTGAC	CAATGACAAA	60
GACACCCCGG	GGCCCAAGAT	CGTCGAAGTA	GTGGCCGGTG	GTGCTGCGCG	GAACGCTGGA	120
GTGCCGAAGG	GGCTCGTTGT	CACCAAGGTC	GACGACCGCC	CGATCAACAG	CGCGGACGCG	180
TTGGTTGCCG	CGGTGCGGTC	CAAAGCGCGG	GGCGCCACGG	TGGCGCTAAC	CTTTCAGGAT	240
CCCTCGGGCG	GTAGCCGCAC	AGTGCAGATC	ACCTCGGCGA	AGGCGGAGCA	GTGATGAAGG	300
TCGCCGCGCA	GTGTTCAAAG	CTCGGATATA	CGGTGGCACC	CATGGAACAG	CGTGGCGAGT	360
TGGTGGTTGG	CGGGGCACTT	GTGCTGCTCG	TTGACGATCG	CACGGCGCAC	GGCGATGAAG	420
ACCACAGCGG	GGCCCTTTGC	ACCGAGCTGC	TCACCGAGGC	CGGGTTTGTG	GTGACGCGCG	480
TGGTGGCGGT	GTGCGCCGAC	GAGGTCGAGA	TCGGAATATC	GCTGAACACA	CGCGTGATCG	540
GCGGGGTGGA	CCTGTTGGTG	TCGGTCGGCG	GGACCGGNGT	GACGNCTCGC	GATGTCACCC	600
CGAAGCCAC	CGNGACATT	CT				622

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCGCAGCGG	TAAGCTGTT	GGCCGCCGCG	ACACTGGTGT	TGACAGCATG	CGGCGGTGGC	60
ACCAACAGCT	CGTCTCAGG	CGCAGGCGGA	ACGTCGGGTG	CGGTGCACTG	CGGCGGCAAG	120
AAGGAGCTCC	ACTCCAGCGG	CTCAGCCGCA	CAAGAAATG	CCATGGAGCA	GTTCGCTCTAT	180
GCTACGTCG	GATCGTGCCC	GGGCTACACG	TGGACTACA	ACGCCAACGG	GTCCGGTGCC	240
GGGGTGACCC	AGTTTCTCAA	CAACGAAACC	GATTTCGCGG	GCTCGGATGT	CCCGTTGAAT	300
CGGTGACCGG	GTCAACCTGA	CGGGTCGGCG	GAGCGGTGCG	GTTCCCGCGC	ATGGGACCTG	360
CGCAGCGGTG	TCGGGCCGAT	CGCGATCACC	TACAATATCA	AGGGCGGTAG	CACGCTGAAT	420
CTTGACGAGC	CCACTACCGC	CAAGATTTTC	AACGGCACCA	TCACCGTGTG	GAATGATCCA	480
CAGATCCAAG	CCCTCAACTC	CGGCACCGAC	CTGCCGCCAA	CACCGATTAG	CGTTATCTTC	540
CGCAGCGACA	AGTCGGGTAC	GTCCGACAAC	TTCCAGAAAT	ACCTCGACGG	TGTATCCAAC	600
GGGGCGTGGG	GCAAAGGCGC	CAGCGAAACG	TTGACGCGGG	GCGTCGGCGT	CGGCGCCAGC	660
GGGAACAACG	GAACGTCGCG	CTACTGCGAG	ACGACCGACG	GGTCGATCAC	CTACAACAGG	720
TGGTCGTTTG	CGGTGGGTAA	GCAAGTTGAAC	ATGGCCCCAG	TCATCACGTC	GGCGGGTCCG	780
GATCCAGTGG	CGATCACCAC	CGAGTCGGTC	GGTAAGACAA	TCGCCGGGGG	CAAGATCATG	840
GGACRAGGCA	ACGACCTGGT	ATTGACACG	TGCTCGTTCT	ACAGACCCAC	CCAGCTGGGC	900
TCTTACCCGA	TCGTGCTGGC	GACCTATGAG	ATCGTCTGCT	CGAAATACCC	GGATGCGAGC	960
ACCGGTACTG	CGGTAAAGGC	GTTTATGCAA	GCCGCGATTG	GTCCAGGCCA	AGAAGGCCTG	1020

GACCAATACG	GCTCCATTCC	GTTCGCCAAA	TCGTTCCAAG	CAAAATTGGC	GGCCGCGGTG	1080
AATGCTATT	CTTGACCTAG	TGAAGGAAT	TCGACGGTGA	GCGATGCCGT	TCCGACAGTA	1140
GGGTGCAAT	TTGGGCGTA	TCAGCTATTG	CGGCTGCTGG	GCCGAGCGCG	GATGGGCGAG	1200

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAAGCAGCT	GCAGGTCGTG	CTGTTGCGAG	AACTGGGCAT	GCCGAAGACC	AAACGCACCA	60
AGACCGGCTA	CACCAACGGAT	GCCGACGCGC	TGCAGTCGTT	GTTCGACAAG	ACCGGGCGATC	120
CGTTTCTGCA	ACATCTGCTC	GCCCAACGCG	ACGTCACCCG	GCTCAAGGTC	ACCCTCGAGC	180
GGTTGCTCCA	AGCGGTGGCC	GCCGACGGCC	GCATCCACAC	CACGTTCAAC	CAGACGAATG	240
CCGCGACCGG	CCGGCTCTCC	TCGACCGAAC	CCAACCTGCA	GAACATCCCG	ATCCGCAACG	300
ACGCGGGCCG	GCGGATCCGG	GACGCGTTCT	TGCTCGGGGA	CGGTTACGCC	GAGTTGATGA	360
CGGCCGACTA	CAGCCAGATC	GAGATGCGGA	TCATGGGGCA	CGTGTCCGGG	GACGAGGGCC	420
TCATCGAGGC	GTTCAACACC	GGGGAGGACC	TGTATTCTGT	CGTCGCGTCC	CGGGTGTTCG	480
GTGTGCCCAT	CGACGAGGTC	ACCGGCGAGT	TGCGGCGCCG	GGTCAAGGCG	ATGTCCTACG	540
GGCTGGTTTA	CGGGTTGAGC	GCCTACGGCC	TGTCGCAGCA	GTTGAAAATC	TCCACCGAGG	600
AAGCCAACGA	GCAGATGGAC	GCGTATTTCG	CCCGATTGCG	CGGGGTGCGC	GACTACCTGC	660
GCGCCGTAGC	GACGCGGGCC	CGCAAGGACG	GCTACACCTC	GACGGTGTCT	GGCCGTGCGC	720
GCTACCTGCT	CGAGCTGGAC	AGCAGCAACC	GTCAGTGC	GGAGGCGCGC	GAGCGGGCGG	780
CGCTGAACGC	GCCGATCCAG	GGCAGCGCGG	CCGACATCAT	CAAGGTGGCC	ATGATCCAGG	840
TCGACAAGGC	GCTCAACGAG	GCACAGCTGG	CGTCGCGCAT	GCTGTGTCAG	GTCCACGAGC	900
AGCTGCTGTT	CGAAATCGCC	CCCGGTGAAC	GCGAGCGGGT	CGAGGCCCTG	GTGCGCGACA	960
AGATGGGCGG	CGCTTACCCG	CTCGACGTCC	CGCTGGAGGT	GTGCTGGGCG	TACGGCCGCA	1020
GCTGGGACGC	GCGCGCGCAC	TGAGTGCCGA	GCGTGATCT	GGGGCGGGAA	TTGCGCGATT	1080
TTTCGCGCCT	GAGTTCACGC	TCGGCGCAAT	CGGGACCGAG	TTGTGTCAGC	GTGTACCCGT	1140
CGAGTAGCCT	CGTCA					1155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

SAGCGCGCTC	TGGTGTGTA	ACGGTTTAC	CGGTGCGCAT	CGGCACGGGC	GTGCGGGGT	60
TCGGGCCTCG	GGTTGGCGAT	CGTCAACAG	GTGGTGTCTA	ACCACGGCGG	ATTGCTCGCG	120
ATCGAAGACA	CCGACCCAGG	CGGCGAGCCC	CCTGGAACGT	CGATTTACGT	GCTGCTCCCC	180
GGCCGCTGCG	TGCCGATTTC	GCAAGTTCCT	GGTGCAGCGG	CTGGCCGCTG	GAGCACGGAG	240
ATCGAGAAT	CTCGGGGTTC	GGCGAAGCTT	ATCTCAGTGG	AATCTCAGTC	CACGCGCGCA	300
ACCTAGTTGT	GCAATTACTG	TTGAAAAGCCA	CACCCATGCC	AGTCACGCA	TGGCCAAGTT	360
GGCCCGAGTA	TGGGGCTAG	TACAGGAAGA	GCAACCTAGC	GACATGACGA	ATCACCCAGC	420
GTATTTCGCA	CGCCGCGAGC	AGCCGGGAAC	CCAGGTTAT	GCTCAGGGGC	AGCAGCAAAC	480
GTACAGCCAG	CAGTTCGACT	GGCGTTACCC	ACCGTCCCGG	CCCCCGGAGC	CAACCCAGTA	540
CCGTCAACCC	TACGAGGCGT	TGGGTGGTAC	CGGGCCGGGT	CTGATACCTG	CGGTGATTCC	600

GACCATGAGC CCCCCCTCTG GATGGTTCG CCAACGCCCT CGTGAGGCA TGTGTGCCAT 660
 CGGCGCGGTT ACAGATAGCGG TGGTGTCCCG CGGCATCGCG GCGCGGCGCC CATCCCTGGT 720
 CGGGTTTCAAC CGGGCAGCCG CCGGCCCCAG CGGCGGCCCA GTGGCTGCCA CGCGCGCGCC 780
 AAGCATCCCC GCAGCAACA TCCCGCCGGG TCCGGTCGAA CAGGTGGCGG CCAAGTGGT 840
 GCGCAGTGCT GTCATGTTGG AAACCGATCT GGGCGCGCAG TCGGAGGAGG GCTCCGGCAT 900
 CATTTCTGCT GCCGAGGGGG TGATCTTGAC CAACAACAC GTGATCGCGG CGGCGGCCAA 960
 GCCTCCCCCTG GGCAGTCCGC CGCGGAAAC GACGTAAC TTTCTGACG GCGCGACCGC 1020
 ACCTTCTACG GTGGTGGGGG CTGACCCAC CAGTGATATC GCCGTCTGTC GTGTTACAGG 1080
 CGTCTCCGGG CTCACCCCGA TCTCCCTGGG TTCTCTCTCG GACCTGAGGG TCGGTGAGCC 1140
 GGTGCTCGGG ATCGGGTTCG CGCTCGGTTT GGAGGGCACC GTGACCAACG GGATCTGTAG 1200
 CGCTCTCAAC CGTCCAGTGT CGACGACCGG CGAGGCGCGG AACCCAGAAC CCGTGTGGGA 1260
 CGCCATTGAG ACCGACGCGG CGATCAACCC CGGTAACCT GGGGCGCGC TGGTGAACAT 1320
 GAACGCTCAA CTCGTCCGAG TCAACTCGCG CATTGCCACG CTGGGCGCGG ACTCAGCCGA 1380
 TGGCGAGAGC GGCTCGATCG GTCTCGGTTT TGGGATTCCA GTCGACCAGG CCAAGCGCAT 1440
 CGCCGACGAG TTGATCAGCA CGGCAAGGCG GTCCATGCCC TCCCTGGGTG TGCAGGTGAC 1500
 CAATGACAAA GACACCCCGG CGCCCAAGAT CGTCSAAGTA GTGGCCGGTG GTGCTGCGCG 1560
 GAACGCTGGA GTGCCGAAGG CGCTCGTGTG CACCAAGGTC GACGACCGCC CGATCAACAG 1620
 CGCGGACGCG TTGGTTGCGG CCGTGCGGTC CAAAGCGCGG GCGCGCACGG TGGCGCTAAC 1680
 CTTTCAAGAT CCTCGGCGG GTAGCCGAC AGTGCAAGTC ACCCTCGGCA AGGCGGAGCA 1740
 GTGATGAAGG TCGCCGCGCA GTGTTCAAG C 1771

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCACCCGCG GTGGCGGCGG CTCTAGAACT AGTGGATCCC CCGGGCTGCA GGAATTGCGC 60
 ACGAGGATCC GAGCTCGCAG GTTGTGCAAC CCGCCGCGCG GGAAGTATCG GTCCATGCGT 120
 AGCCCCGGCA CGGCGAGCGC CGGAATGGCG CGAGTGAGGA GCGCGGCAAT TTGGCGGGGC 180
 CCGGCGAGCG CGAGCGCGCG AATGGCGCGA GTGAGGAGCG GGCAGTCTAT GCCCAGCGTG 240
 ATCCAATCAA CCTGCATTG CGCTGCGGGC CCAATTTGACA ATCGAGGTAG TGAGCGCAAA 300
 TGAATGATGG AAAACCGGGCG GTGACGTCCG CTGTTCTGGT GGTGCTAGGT GCCTGCGCTGG 360
 CGTGTGGGCT ATCAGGATGT TCTTCCGCGA AACCTGATGC CAGGGAACAG GGTGTCTCCG 420
 TGAGCCGAC GGCCTCCGAC CCGCGCTCC TCGCCGAGAT CAGGCAGTGT CTTGATGCGA 480
 CAAAAGGGTT GACCAGCGTG CACGTAGCGG TCCGAACAAC CCGGAAAGTC GACAGCTTGC 540
 TGGGTATTAC CAGTGCCGAT GTCCGAGTCC GGGGCAATCT GCTCGCGGCA AAGGGCGTAT 600
 GCACCTACAA CGACGAGCAG GGTGTCCCGT TTCGGGTACA AGGCAGCAAC ATCTCGGTGA 660
 AACTGTTGCA CGACTGGAGC AATCTCGGCT CGATTTCTGA ACTGTCAACT TCACGCGTGC 720
 TCGATCTCTG CGCTGGGGTG ACGCAGCTGC TGTCCGGTGT CACGAACCTC CAAGCGCAAG 780
 GTACCGAGAT GATAGACGGA ATTTGACCA CCAAAATCAC CCGGACCATC CCGCGAGGT 840
 CTGTCAAGAT GCTTGATCCT GCGGCCAAGA GTGCAAGGCC GCGACCCGTG TGGATTGCC 900
 AGGACGGCTC GCACCACTCT GTCCGAGCGA GCATCGACCT CGGATCCGGG TCGATTGACG 960
 TCACGCGAGT GAAATGGGAA GAACCCGTCA ACCTGCACTA GGCGCAAGTT GCGTCGACG 1020
 GTTGTGCGAA ACGCCCTTGT GAACGGTGTC AACCGNAC 1058

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA	CGAGAGGTGA	TCGACATCAT	CGGGACCAGC	CCCACATCGT	GGGAACAGGC	60
GGCGGGCGAG	GGGTCACAG	GGGCGCGGGA	TAGCGTCGAT	GACATCCGCG	TCGCTCGGGT	120
CATTGACGAG	GACATGGCCG	TGGACAGCGC	CGGCAAGATC	ACCTACCGCA	TCAAGCTCGA	180
AGTGTCTGTC	AAGATGAGGC	CGGCGCAACC	CGCTAGCAC	GGGCCGCGGA	GCAAGACGCA	240
AAATCGCAGC	GTTTGCGGTT	GATTCTGTGC	ATTTTGTGTC	TGCTCGCCGA	GGCTTACCAG	300
GCGCGGCCCA	GGTCCGCGTG	CTGCCGTATC	CAGGCGTGCA	TCGCGATTCC	GGCGGCCACG	360
CCGGAGTTAA	TGCTTCGCGT	CGACCCGAAC	TGGGCGATCC	GCCGNGAGC	TGATCGATGA	420
CCGTGGCCAG	CCGTCGATG	CCCGAGTTGC	CCGAGGAAAC	GTGCTGCCAG	GCCGGTAGGA	480
AGCGTCCGTA	GGCGGCGGTG	CTGACCGGCT	CTGCCTGCGC	CCTCAGTGCG	GCCAGCGAGC	540
GG						542

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 913 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGTGCGGCC	CGCGCTCCG	TTGCCOCCAT	TGCCGCGCTC	GCCGATCAGC	TGCGCATCGC	60
CACCATCACC	CGCTTTGCGC	CGGGCACCGC	CGGTGCGGCC	GGGGCCGCGC	ATGCCACCGC	120
TTGACCTTGG	CGCGCGCGCG	CGCCATTGCC	ATACAGCAC	CCGCGGGGGG	CACCGTTACC	180
GCCGTGCGCA	CCGTGCGCGC	CGCTGCCGTT	TCAGGCCGGG	GAGGCCGAAT	GAACCCCGGC	240
CAAGCCCGCC	GCGGACACCG	TTGCCGCTT	TTCCGCGCGC	CCGCGCGCGC	CCGCCAATTG	300
CCGAACAGCC	AMGCACCGTT	GCCGCCAGCC	CCGCGCGCGT	TAAAGCGCGT	GCCGGGCGCC	360
GCCCGCGGAC	CGCCATTAC	CGCGTTTCCC	GTTCTGTGCC	CCGCCGTTAC	CGGCGCCGCC	420
GTTTGCGGCC	AATATTCTGG	GGGCACCGCC	AGACCCGCGC	GGGCCACCAT	TGCCCGCGGG	480
CACCGAAACA	ACAGCCCAAC	GGTGCCGCGC	GCCCGCGCGT	TTGCCGCGAT	GCGCGCCCAT	540
TCACCCGCGC	CACCGCGGTT	AATGTTTATG	AACCCGCTAC	CGCCAGCGCG	GCCCTTATTG	600
CCGGGCGCGC	GAGNGCGTGC	CGCGCGCGCG	CGCCAACCGC	CAAAAGCCCG	GGGTGTCCAC	660
CGGCCCCGCG	GAGGCCACCG	GTCCGCGCGA	TCCCCCGGTT	GCCGCGCGGT	CCGCGGCCAT	720
TGGTGCTGCT	GAAGCGGTTA	GCGCGCGTTC	CGCSGGTTCC	GGCGGTGGCG	CNTGGCGCGC	780
CGGCCCCGCG	GTTGCGGTAC	AGCCACCCCC	CGGTGCGGCC	GTTGCGGCCA	TTGCCCGCAT	840
TGCGCGCGTT	GCCGCCATTG	CGGCGGTTCC	CGCGGCCACC	GCCGCGTTGG	CGCGCGGCGC	900
CGCGCGCGCG	CGC					913

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1872 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACGTTG	GTGTAGAAAA	ATCCTGCCGC	CCGACCCTTT	AAGGCTGGGA	CAATTTCTGA	60
TAGCTACCCC	GACACAGGAG	GTTACGGGAT	GAGCAATTCG	CGCCGCGCGT	CACCTAGGTTG	120

GTCATGGTTG CTGAGCGTGC TGGCTGCGGT CGGGCTGGGC CTGGCCACGG CGCCGGGCCA 180
 GCGCGCCCCG CCGGCCCTGT GCGAGGACCG GTTCGCCGAC TTCCCGCGCG TGCCCTCTCA 240
 CCGGTCGCGG ATGGTCGCCCC AAGTGGCGCC ACAGGTGGTC AACATCAACA CCAAACTGGG 300
 CTACAACAAC GCGCTGGGCG CCGGGACCGG CATCGTCATC GATCCCAACG GTGTGCTGCT 360
 GACCAACAAC CACGTGATCG CGGGCGCCAC CGACATCAAT GCGTTCAACG TCGGCTCCGG 420
 CCAAACTGAC GCGCTCGATG TGGTCGGGTA TGACCGACCC CAGGATGTGC CGGTGCTGCA 480
 GCTCGCGCGT GCGCGTGGCC TGCCGTGCGG GGCATCGGT GCGCGCGCTC GCGTGGTGA 540
 GCCCGTCTGT GCGATGGGCA ACAGCGGTGG GCGAGGCGGA ACGCCCGCTG CCGTGCCTGG 600
 CAGGGTGGTC GCGCTCGGCC AAACCGTGCA GCGCTCGGAT TCGCTGACCG GTGCCGAAGA 660
 GACATTGAAC GGGTTGATCC AGTTGATGTC CGCAATCCAG CCGCGTGATT CGGGCGGGCC 720
 CGTCGTCAAC GGCCTAGGAC AGGTGGTCGG TATGAACACG GCGCGTCCCG ATAACCTCCA 780
 GCTGTCCGAG GGTGGGCGAG GATTGCGCAT TCCGATCGGG CAGGCGATGG CGATCGCGGG 840
 CCAAACTCGA TCGGGTGGGG GGTACCCAC CGTTTCATATC GGGCTTACCG CCTTCCTCGG 900
 CTTGGGTGTT GTCGACACCA ACGGCAACCG CGCACGAGTC CAACGCGTGG TCGGAAGCCG 960
 TCCGCGCGCA AGTCTCGGCA TCTCCACCG CGACGTGATC ACCGCGGTGC ACGGCGCTCC 1020
 GATCAACTCG GCCACCGCGA TGGCGGACCG GCTTAACGGG CATCATCCCG GTGACGTCAT 1080
 CTCGCTGAAC TGGCAAAACG AGTCGGGCGG CACGCGTACA GGGAACTGTA CATTTGCCGA 1140
 GGGACCCCGG GCGCTGATTG TCGCGGATAC CACC CGCGCG GCGGCCAATT GGATTGGGCG 1200
 CAGCGCTGAT TGGCGCGTGA GCCCCGAGT TCCGTCTCCC GTGCGCGTGG CATTTGGGAA 1260
 GCAATGAACG AGGCGAGTGA CAGCGTTGAG CACCCTCCG TGCAGGGCAG TTAGCTCGAA 1320
 GCGCGTGTGG TCGAGCATCC GGATGCCAAG GACTTCGGCA GCGCGCGCGC CTCTCCCGCC 1380
 GATCCGACCT GGGTTAAGCA CGCCGTCTTC TACGAGGTGC TGGTCCGGGC GTTCTTCGAC 1440
 CGCAGCGCGG ACGGTTCCGN CGATCTCGGT GGACTCTAGC ATCGCTCTGA TCACTTCGAG 1500
 TGGCTGGCA TCGACTGCAAT CTGTTGCCCG CGTTCTCAGC ACTCACCGCT GCGCGACGCG 1560
 GGTTACGACA TTGCGGACTT CTACAAGGTG CTGCCCGAAT TCGGCACCGT CGACGATTTT 1620
 GTCCCGCTGG TCGACACCGC TCACCGCGCA GGTATCCGCA TCATCACCGA CTCTGGTGATG 1680
 AATCACCTCT CGGAGTCGCA CCCCTGGTTT CAGGAGTCCC CGCGGACCC AGACGGACCG 1740
 TACGCTGACT ATTAAGTGTG GAGCGACACC AGCGAGCGCT ACACCGACGC CCGGATCATC 1800
 TTCGTCGACA CCGAAGAGTC GAATCGGTCA TTCGATCCTG TCCGCGGACA GTTNTACTAG 1860
 GCACCGATTCT TT

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCCGCGAA ACCTGATGCC GAGGAACAGG GTGTTCCCGT GAGCCCGAAG CGGTCCGACC 60
 CGCGCTCTCT CGCGAGATAC AGCGAGTCGG TTGATGCGAC AAAAGGTTTG ACCGAGCTGC 120
 ACGTAGCGGT CCGAACAACC GGGAAAGTCG ACAGCTTGCT GGGTATTACC AGTGCCGATG 180
 TCGACGTTCG GGGCAATCCG CTCGCGGCAA AGGGCGGTATG CACCTACAAAC GACGAGCAGG 240
 GTGTCCCGGT TCGGGTACAA GCGACACAAC TCTCGGTGAA ACTGTTTCGAC GACTTGGGCA 300
 ATCTCGGCTC GATTTCGTAA CTGTCAACTT CACGCGTGCT CGATCTCTGC GCTGGGGTGA 360
 CGCAGCTGCT GTCCGCTGTC ACGAACCCTC AAGCGCAAGG TACCGAAGTG ATAGACGGAA 420
 TTTGACCAC CAAAATCCCG GGGACCATCC CCGGAGCTTC TGTCAGATGT CTTGATCCTG 480
 GCGCGCAAGG TGCAAGGCCG GCGACCGTGT GGATTTGCCA GGCAGGCTCG CACCACTCTG 540
 TCCGAGCGAG CATCGACCTC GGATCCGGGT CGATTGAGCT CACGCGAGTC AAATGGAACG 600
 AACCCTGCAA CGTCGACTAG GCGCAAGTTG CGTCGACGGC TTGCTCGAAA CGCCCTTTGTG 660
 AACGCTGTCA ACGGCACCG AAAAAGTGAAC CCGTACGCGC ATCTGAAAAT TGACCCCTTA 720
 GACCGGGCGG TTGGTGGTTA TTCTCGGCTG GTTCCGGCTG GTGGGACGCG GCCGAGGTGC 780
 CGGTCTTTGA GCGGATGAGT GTCGCTTTG AGGGCGACGA CTTGAGCATG GTGGACGAGG 840

CGGTGCGATCA	TGGCGGCAGC	AACGACGTGC	TGCGCGCCGA	AAACCTCGCC	CCACCGGCCG	900
AAGGCTTAT	TGGACGTGAC	GATCAAGCTG	GCCCCTCAT	ACCGGGAGGA	CACGAGCTGG	960
AAGAGAGGT	TGGCGGCCTC	GGGCTCAAAC	GGAATGTAAC	CGACTTCGTC	AACCACGAGG	1020
AGCGGATAGC	GGCCAAACCG	GGTGAGTTGC	GCGTAGATGC	GCCCGCGGTG	GTGAGCCTCG	1080
GCGAACCGTG	CTACCCATTC	GGCGGCGGTG	GCGAACAGCA	CCCGATGACC	GGCCTGACAC	1140
GCGGTATCG	CCAGGGCCAG	CGCAAGATGA	GTCTTCCCG	TGCCAGGCGG	GGCCCCAAAA	1200
CACGACGTTA	TCCGCGGCGG	TGATGAAATC	CAGGGTGCCC	AGATGTGCGA	TGGTGTGCGG	1260
TTTGAGGCCA	CGAGCATGCT	CAAAGTCGAA	CTCTTCCAA	GACTTCCGAA	CCGGGAAGCG	1320
GCGGCGCGG	ATGCGGCCCT	CACCACCATG	GGACTCCCGG	GCTGACACTT	CCCGCTGCAG	1380
GCGGCGGCC	AGGTATTCTT	CGTGCTCCA	GTCTCGGCG	CGGCGCGCAT	CGGCACGCCG	1440
GGACACTGAC	TCACGCGAGG	TGGGAGCTTT	CAATGCTCTT	GT		1482

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCA	CGAGCCGGCG	ATAGCTTCTG	GGCGCGGCC	GACCAGATGG	CTCGAGGGTT	60
CGTGCTCGGG	GCCACCGCGC	GCGCACCAAC	CCTGACCGGT	GAGGGCCCTGC	AACACGCCGA	120
CGGTCACTCG	TTGCTGCTGG	ACGCCAACAA	CCCGGCGGTG	GTTCCTTAGC	ACCCGGCCTT	180
CGCCTACGAA	ATCGGCTACA	TCGNGGAAAG	CGGACTGGCC	AGGATGTGCG	GGGAGAACCC	240
GGAGAAGCTC	TTCTTTCTACA	TCACCGTCTA	CAACGAGCCG	TACGTGCAGC	GCCCGGAGCC	300
GGAGAAGCTC	GATCCCGAGG	GCGTGCTGGG	GGGTATCTAC	CGNTATCACG	CGGCCACCGA	360
GCAACGCACC	AACAAGGNGC	AGATCCTGGC	CTCCGGGGTA	GCGATGCCCG	CGCGCTGCG	420
GGCAGCACAG	ATGCTGGCGG	CCGAGTGGGA	TGTCGCCGCC	GACGTGTGGT	CGTGACCAG	480
TTGGGGCGAG	CTAAACCGCG	ACGGGGTGGT	CATCGAGACC	GAGAAGCTCC	GCCACCCCGA	540
TCGGCGGGCG	GGCGTGCCCT	ACGTGACGAG	AGCGCTGGAG	AATGCTCGGG	GCCCGGTGAT	600
CGCGGTGTGC	GACTGTGATC	GCGCGTCCC	CGAGCAGATC	CGACCGTGGG	TGCGGGCGAC	660
ATACCTCACG	TTGGGCACGC	ACGGGTTGCG	TTTTTACGAC	ACTCGGCCCG	CCGGTCTGCT	720
TTACTTCAAC	ACCGACGCGG	AATCCCAGGT	TGGTCGCGGT	TTTGGGAGGG	GTGGCCCGGG	780
TCGACGGGTG	AATATCGACC	CATTGCTGTC	CGGTCTGGGG	CCGCCCGCCC	AGTTACCCGG	840
ATTTCGAGAA	GGTGGGGGCT	TGCGCCCGAN	TAAGTT			876

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCCCCCGG	GCTGCAGGAA	TTCCGCACGA	GAGACAAAT	TCCACGCGTT	AATGCAGGAA	60
CAGATTTCAT	ACGAATTCAC	AGCGGCACAA	CAATATGTGC	CGATCGCGGT	TTATTTCGAC	120
AGCGAAGACC	TGCCGCAAGT	GGCGAAGCAT	TTTTACAGCC	AAGCGGTTCGA	GGAACGAAAC	180
CATGCAATGA	TGCTCGTGCA	ACACCTGCTC	GACCGCGACC	TTCTGTGTCGA	AATTTCCCGGC	240
GTAGACACGG	TGCGAAACCA	GTTCGACAGA	CCCGCGAGG	CAGTGGCGCT	CGCGCTCGAT	300
CAGGAACGCA	CAGTACCGGA	CCAGGTGCGT	CGGCTGACAG	CGGTGGCCCG	CGACGAGGGC	360
GATTTCCTCG	GCGAGCAGTT	CATGACGTGG	TTCTTGCAGG	AACAGATCGA	AGAGGTGGCC	420

TTGATGGCAA	CCCTGGTGCG	GGTTGCCGAT	CGGGCCGGGG	CCAACCTGTT	CGAGCTAGAG	480
AACTTCGTCG	CACGTGAAGT	GGATGTGGCG	CCGGCCGCAT	CAGGCGCCCC	GCACGCTGCC	540
GGGGGCCGCC	TCTAGATCCC	TGGGGGGGAT	CAGCGAGTGG	TCCCGTTCGC	CCGCCCGTCT	600
TCCAGCCAGG	CCTTGGTGCG	GCCGGGGTGG	TGAGTACCAA	TCCAGGCCAC	CCCGACCTCC	660
CGNNAAGT	CGATGTCCTC	GTACTCATCG	ACGTTCCAGG	AGTACACCCG	CCGGCCCTGA	720
GCTGCCGAGC	GGTCAACGAG	TTGCGGATAT	TCCTTTAACG	CAGGCAGTGA	GGGTCCCACG	780
GCGGTTGGCC	CGACCCGCGT	GGCCGCACTG	CTGGTCCAGT	ATCGGGGGGT	CTTGGCGAGC	840
AACAACGTCG	CGAGGAGGGG	TGGAGCCCGC	CGGATCCGCA	GACCGGGGGG	GCGAAAACGA	900
CATCAACACC	GCACGGGATC	GATCTGCCGA	GGGGGGTGGC	GGAATACCGA	ACCGTGTAG	960
GAGCGCCAGC	AGTTGTTTTT	CCACCAGCGA	AGCGTTTTTC	GGTCATCGGN	GGCNNTTAAG	1020
T						1021

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTGCCGAGC	AACGGAAGAA	CACAACCATG	AAGATGGTGA	AATCGATCGC	CGCAGGTCGTG	60
ACCGCCGCGG	CTGCAATCGG	CGCCGCTGCG	GCCGGTGTGA	CTTCGATCAT	GGCTGGCGGN	120
CCGGTCGTAT	ACCAGATGCA	GCCGGTCGTC	TTCCGGCCGC	CACGCGCGTT	GGACCCCGNA	180
TCCGCCCTTG	ANGTCCCGAC	CGCCGCCAG	TGGACCAGNC	TGCTCAACAG	NCTCGNCGAT	240
CCCAACGTGT	CGTTTNGNAA	CAAGGGNAGT	CTGTGTCGAG	GNGGNATCGG	NGGNANCGAG	300
GGNGNGNATC	GNCGANCA	A				321

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATCGGT	TCCGGTTGGC	GACGGGTTTT	GGNGCGGGT	GGTTAACCCG	CTCGGCCAGC	60
CGATCGACGG	GCGCGGAGAC	GTCGACTCCG	ATACTCGCGG	CGCGCTGGAG	CTCCAGGCGC	120
CCTCGGTGAT	GNACCCGCAA	GGCGTGAAGG	AGCCGTTGNA	GACCGGGATC	AAGGCGATTG	180
ACGCGATGAC	CCCGATCGGC	CGCGGGCAGC	GCCAGCTGAT	CATCGGGGAC	CGCAGACCCG	240
GCAAAACCCG	CCGCTCTGTG	CGGACACCAT	CCTCAAACCA	GCGGGAAGAA	CTGGGAGTCC	300
GGTGATCCC	AAGAAGCAGG	TGCCTTGTG	TATACGTTGG	CCATCGGGCA	AGAAGGGGAA	360
CTTACCATCG	CCG					373

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACGCCGT	GATGGGATTC	CTGGGCGGGG	CCGGTCCGCT	GGCGGTGGTG	GATCAGCAAC	60
TGGTTACCCG	GGTGCCGCAA	GGCTGGTCTG	TTGCTCAGGC	AGCCGCTGTG	CCGTTGGTGT	120
TCTTTGACGC	CTGGTACGGC	TTGGCCGATT	TAGCCGAGAT	CAAGCGGGC	GAATCGGTGC	180
TGATCCATGC	CGGTACCGGC	GGGTGGGGCA	TGGCGGCTGT	GCAGCTGGCT	CGCCAGTGGG	240
GCCTGGAGGT	TTTCGTACCC	GCCAGCCGTG	GNAAGTGGGA	CACGCTCGGC	GCCATNGNGT	300
TTGACGACGA	NCCATATCCG	NGATTCCNC	ACATNCGAAG	TTCCGANGGA	GA	352

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCCGCG	TTCATTCCGT	TCGACCAGCG	GCTGGCGATA	ATCGACGAAG	TGATCAAGCC	60
GCGGTTCCGC	GCGCTCATGG	GTCACAGCGA	GTAATCAGCA	AGTTCTCTGG	TATATCGCAC	120
CTAGCGTCCA	GTGTGCTTGC	AGATCGCTTT	CGTACCGTCA	TCGCATGTAC	CGGTTCCGCT	180
GCCGCACGCT	CATGCTGGCG	GCGTGCATCC	TGGCCACGGG	TGTGGCGGGT	CTCCGGGTGC	240
GCGCGCAGCT	CGCAGCCCAA	ACCGCGCCGG	TGCCCGACTA	CTACTGGTGC	CCGGGGCAGC	300
CTTTGCAGCC	CGCATGGGGG	CCCAACTGGG	ATCCCTACAC	CTGCCATGAC	GACTTCCACC	360
CGCAGCAGCC	CGGCCCGGAC	CACAGCCGCG	ACTACCCCGG	ACCCATCCTC	GAAGTCCCGC	420
TGCTTGACGA	TCCCGGTGCT	GCGCCGCCGC	CCCGGCTGCT	CGGTGGCGGC	GCATAGCGCT	480
CGTTGACCGG	GCCGATCAG	CGAATACCGG	TATAAACCCG	GGCGTGCCCC	CGGCAAGCTA	540
CGACCCCCCG	CGGGGCAGAT	TTACGCTCCG	GTGCCGATGG	ATCGCGCCGT	CCGATGACAG	600
AAAATAGGCG	ACGGTTTTGG	CAACCGCTTG	GAGGACGCTT	GAAGGGAACC	TGTCATGAAC	660
GGCGACAGCG	CTCCACCAT	CGACATCGAC	AAGGTTGTGA	CCCGCACACC	CGTTGCCCGG	720
ATCGTG						726

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGACGACG	ACGAACGTCG	GGCCACCACC	CGCCTATGCG	TTGATGCAGG	CGACCGGGAT	60
GGTGCCCGAC	CATATCCAAG	CATGCTGGGT	GCCCACTGAG	CGACCTTTTG	ACCAGCCGGG	120
CTGCCCGATG	GCGGCCCGGT	GAAGTCATTG	GCGCGGGGCT	TGTGCACCTG	ATGAACCCGA	180
ATAGGGAACA	ATAGGGGGGT	GATTTGGCAG	TTCAATGTCT	GGTATGGCTG	GAAATCCAAT	240
GGCGGGGCTC	GCTCGGCGCC	GACCAGGCTC	GCGCAGGCGG	GCCAGCCCGA	ATCTGGAGGG	300
AGCACTCAAT	GGCGGGCATG	AAGCCCCGGA	CGGCGCAGCG	TCCTTTGGAA	GCAACTAAGG	360
AGGGGCGCGG	CATTTGTATG	CGAGTACCAC	TTGAGGGTGG	CGGTCCGCTG	GTCTCGAGC	420
TGACACCCGA	CGAAGCCCGC	GCACTGGGTG	ACGAACCTCA	AGGCGTTACT	AGCTAAGACC	480
AGCCCAACGG	CGAATGGTCG	GCGTTACGCG	CACACCTTCC	GGTAGATGTC	CAGTGTCTGC	540
TGCGCATGT	ATGCCGAGGA	GAACCTTTGG	ATACAGCGCT			580

(2) INFORMATION FOR SEQ ID NO:26:

10084843.022502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGGAGCG	CGGGGGTTT	TGGCGGGGCC	GGGCGGTGC	GCGGCAACGG	CGGGCGGGC	60
GGTACCGCG	GGTTGTTCCG	TGTCGGCGGG	GCCGCTGGGG	CCGGAGGCAA	CGGCATCGCC	120
GGTGTCACG	GTACGTCGGC	CAGCACACCG	GGTGGATCCG			160

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACCGATA	CGATGGTGAT	GTACGCCAAC	GTTGTCGACA	CGCTCGAGGC	GTTACAGTAC	60
CAGCGCACAC	CCGACGGCGT	GACCATCGGC	GATCGGGCCC	CGTTCGCGGA	GGCGGCTGCC	120
AAGGCGATGG	GAATCGACAA	GCTGCGGGTA	ATTCATACCG	GAATGGACCC	CGTCGTCGCT	180
GAACCGGAAC	AGTGGGACGA	CGGCAACAAC	ACGTTGGCGT	TGGCGCCCGC	TGTCGTTGTC	240
GCCTACGAGC	GCAACGTACA	GACCAACGCC	CG			272

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCAGCCGGTG	GTCTCGGAC	TATCTGCGCA	CGGTGACGCA	GCGCGACGTG	CGCGAGCTGA	60
AGCGGATCGA	GCAGACGGAT	CGCTGCGCG	GGTTCATGCG	CTACCTGGCC	GCTATCACCG	120
CGCAGGAGCT	GAACGTGGCC	GAAGCGGCG	GGGTGATCGG	GGTCGACGCG	GGGACGATCC	180
GTTCGGATCT	GGCGTGTTTC	GAGACGGTCT	ATCTGGTACA	TCCGCTGCCC	CGCTGGTCGC	240
GGAATCTGAC	CGCGAAGATC	AAGAAGCGGT	CAAGATCCA	CGTCGTCGAC	AGTGGCTTCG	300
CGGCCTGGTT	GCGCGGG					317

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

205220.4618001

GATCGTGGAG CTGTCGATGA ACACGCTTGC CGGACGCGCG GCGGCCACGA CGTCGGTGTA 60
 GCAGCGCGCG ACCACCTCGC CGGTGGGCAG CATGGTGATG ACCACGTCGG CCTCGGCCAC 120
 CGCTTCGGGC GCGCTACGAA ACACGCGCAC ACCGTGCGCG GCGCGCCGCG ACSCGCCCGT 180
 GG 182

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCGCGAAG TTTGGTGAGC AGGTGGTCTGA CGCGAAAGTC TGGGCGCCTG CGAAGCGGGT 60
 CGGCGTTTAC GAGGCGGAAGA CACGCCCTGTC CGAGCTGCTG CGGCTCGTCT ACGGCGGGCA 120
 GAGGTTGAGA TTGCCCGCGC CGCGGAGCCG GTAGCAAAGC TTGTGCCGCT GCATCCTCAT 180
 GAGACTCGCG GGTTAGGCTA TGACCATGGC GTCTACCGCG TGCCCCACGA TTTGGACGCT 240
 CCGTTGTCTAG ACGACGTGCT CGAACGCTTT CACCGGTGAA GCGCTACCTC ATCGACACCC 300
 ACGTTTGG 308

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCGACGACGA GCAACTCAGC TGGATGATGG TCGGCAGCGG CATTGAGGAC GGAGAGAATC 60
 CGGCCGAAGC TGCCGCGCGG CAAGTGCTCA TAGTGACCGG CCGTAGAGGG CTCCCCCGAT 120
 GGCACCGGAC TATTTCTGGT TGCCGCTGGC CGGTAAGAGC GGGTAAAGAA ATGTGAGGGG 180
 ACACGATGAG CAATCACACC TACCGAGTGA TCGAGATCGT CGGGACCTCG CCCGACGCGG 240
 TCGACGCGCG AATCCAGGGC GGTCTGG 267

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCGTGCCGA AAGAATGTGA GGGGACACGA TGAGCAATCA CACCTACCGA GTGATCGAGA 60
 TCGTCGGGAG CTCGCCCGAC GCGCTCGACG CGGCAATCCA GGGCGGTCTG GCCCGAGCTG 120
 CGCAGACCAT GCGCGCGCTG GACTGGTTTG AAGTACAGTC AATTGAGGC CACCTGGTGG 180
 ACGGAGCGGT CGCGCACTTC CAGGTGACTA TGAAGTCGG CTTCGCGTGG AGGATTCCTG 240
 AACCTTCAAG CGCGGCCGAT AACTGAGGTG CATCATTAAG CGACTTTTTC AGAACATCCT 300
 GACGCGCTCG AAACGCGGTT CAGCCGACGG TGGCTCGGCC GAGGCGCTGC CTCCAAATCT 360
 CCTGCGACAA TTCGTCGGCG GCGCCTACAA GGAAGTCGGT GCTGAATTGC TCGGGTATCT 420

10084843.022502

GGTCGACCTG	TGTGGGCTGC	AGCCGGACGA	AGCGGTGCTC	GACGTGCGCT	GC GGCTCGGG	480
GCGGATGGCG	TTGCCGCTCA	CCGGCTATCT	GAACAGCGAG	GGACGCTACG	CCGGCTCTGA	540
TATCTCGCAG	AAAGCCATCG	CGTGGTGCCA	GGAGCACATC	ACCTCGGCCG	ACCCCAACTT	600
CCAGTTCGAG	GTCTCCGACA	TCTACAATC	GCTGTACAAC	CCGAAAGGGA	AATACCAGTC	660
ACTAGACTTT	CGCTTTCCAT	ATCCGGATGC	GTGCTTCGAT	GTGGTGTTTC	TTACCTCGGT	720
GTTCACCAC	ATGTTTTCGC	CGGACGTGGA	GCACTATCTG	GACGAGATCT	CCCGCGTGCT	780
GAAGCCCGGC	GGACGATGCC	TGTGCACGTA	CTTCTTGCTC	AATGACGAGT	CGTTAGCCCA	840
CATCGCGGAA	GGAAAGAGTG	GACACAATC	CACGACATGAG	GGACCCGGGT	ATCGGACACT	900
CCACAAGAA	CGGCCCGAAG	AAGCAATCGG	CTTGCCGGAG	ACCTTCGTCA	GGGATGTCTA	960
TGGCAAGTTC	GGCCTCGCCG	TGCACGAACC	ATTGCACTAC	GGCTCATGGA	GTGGCCGGGA	1020
ACCACGCCTA	AGCTTCCAGG	ACATCGTCAT	CGCGACCAA	ACCGCGAGCT	AGGTCCGCAT	1080
CCGGGAAGCA	TCGCGACACC	GTGGCGCCGA	GCGCGCGTGC	CGGCAGGCCG	ATTAGGCGGG	1140
CAGATTAGCC	CGCCCGCGCT	CCCGGCTCCG	AGTACGGCGC	CCCGAATGGC	GTCAACGGCT	1200
GGTAACCACG	CTTGCGCGCC	TGGGCGGCGG	CCTGCGCGAT	CAGGTGGTAG	ATGCCAGCAA	1260
AGCTCGCTG	ATCGGTCATC	ACCAACGGTG	ACAGCAGCCG	GTGTGCAACC	AGCGGGAACG	1320
CCACCCCGGT	CTCCGGTCT	GTCCAGCCGA	TCGAGCCGCC	CAAGCCCCCA	TGACCAAACC	1380
CCGCGATCAG	GTTCGCGCAT	GGCATACCGT	GATAGCCAA	ATGAAAATT	AAGGGCAACA	1440
ATAGATTTCG	ATCCGGGACA	ACTTGGCGTC	GGTTGCGGCT	CAGGCCCGTG	ACCAGTCTCC	1500
CGCACAAGAA	CCGTATGCCG	TGATCTCGC	CTCGTGCCG			1539

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCAGGGTG	CGGTGGATGA	GCGTCACCGC	GGGGCAGGCC	GAGCTGACCG	CCGCCCAGGT	60
CCGGGTGTCT	GCGGCGGCCT	ACGAGACGGC	GTATGGGCTG	ACGGTGCCCC	CGCCGGTGAT	120
CGCGGAGAAC	CGTGCTGAAC	TGATGATTCT	GATAGCGACC	AACCTCTTGG	GGCAAAACAC	180
CCCGCGGATC	GCGGTCAACG	AGGCCGAATA	CGCGGAGATG	TGGGCCCAAG	ACGCGCCCGC	240
GATGTTTGGC	TAGCCGCGCG	CGACGGCGAC	GGCGACGGCG	ACGTTGTCTG	CGTTTCGAGGA	300
GGCGCCGGAG	ATGACCAGCG	CGGGTGGGCT	CCTCGAGCAG	GCCCGCCGCG	TCGAGGAGGC	360
CTCCGACACC	GCGCGGCGCA	ACCAATTGAT	GAACRAATGT	CCCCAGGCCG	TGAAACAGTT	420
GGCCACGCC	ACGCAGGGCA	CCACGCCTTC	TTCCAAGCTG	GGTGGCCTGT	GGAAAGACGT	480
CTCGCCGAT	CGGTTCGCCA	TCAGCAACAT	GGTGTGATG	GCCAACAACC	ACATGTCGAT	540
GACCAACTCG	GGTGTGTCGA	TGACCAACAC	CTTGAGCTCG	ATGTTGAAGG	GCTTTGCTCC	600
GCGCGCGCC	GCCACGGCGG	TGCAAAACCG	GGCGCAAAAC	GGGGTCCGGG	CGATGAGCTC	660
GCTGGGCAGC	TCGCTGGGTT	CTTCGGGTCT	GGCGGTGGG	GTGGCCGCCA	ACTTGGGTGC	720
GGCGGCTCG	GTACGGTATG	GTCAACGGGA	TGGCGGAAAA	TATGCANAGT	CTGGTCGGCG	780
GAACGCTGGT	CCGGCGTAAG	GTTTACCCCC	GTTTTCGTGA	TGCGGTGAAC	TTGCTCAACG	840
GAAACAGTTA	C					851

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCGATCGG	GCGGAAATTT	GGACCAGATT	CGCCTCCGGC	GATAACCCAA	TCAATCGAAC	60
CTAGATTTAT	TCCGTCAGG	GGCCCGAGTA	ATGGCTCGCA	GGAGAGGAAC	CTTACTCGTG	120
CGGGCACCTG	TGCTAGGTCC	TCGATACGGC	GGAGAGCGTC	GACATTTTCC	ACCGACACCC	180
CCATCCAAAC	GTTCGAGGGC	CACCTCCAGCT	TGTGAGCGAG	GCGACGCACT	CGCAGGCTGC	240
GCTTGGTCAA	GATC					254

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCCTGACC	GAAGCGGCGC	CGCCCAAGGC	GAAGTCGCTG	TTGGACCAGG	AGGGACGGGA	60
CGATCTGGCG	CTGCGGATCG	CGGTTCAAGC	GGGGGGGTGC	GCTGGATTGC	GCTATAACCT	120
TTCTTCGAC	GACCCGAGCG	TGGATGGTGA	CCAAACCGCG	GAGTTCGGTG	GTGTCAGGTT	180
GATCGTGGAC	CGGATGAGCG	CGCCGTATGT	GGAGAGCGCG	TCGATCGATT	TCGTGCACAC	240
TATTGAGAAG	CAAGGTTTAC	CATCGACAAT	CCCAACGCCA	CCGGCTCTCT	CGCGTCGCGG	300
GATTTCGTTCA	ACTGATAAAA	CGCTAGTACG	ACCCCGCGGT	GCGCAACACG	TACGAGCACA	360
CCAAAGACCTG	ACCGCGCTGG	AAAAGCAACT	GAGCGATGCC	TTGCACCTGA	CCGCGTGGCG	420
GGCCGCCGGC	GGCAGGTGTC	ACCTGCATGG	TGAACAGCAC	CTGGGCCCTGA	TATTGCGACC	480
AGTACACGAT	TTTGTGATC	GAGGTCACTT	CGACCTGGGA	GAAGCTGCTG	CGGAACGCGT	540
CGCTGCTCAG	CTTGGCCAAG	GCCTGATCGG	AGCGCTTGTG	GCGCACGCGG	TCGTGGATAC	600
GCGCACAGCG	ATTGCGAAGC	ATGTTGTCCA	CATCGCGGTT	CTCCAGCGCG	TTGAGGTATC	660
CTGAATCGC	GGTTTTGGCC	GGTCCCTCCG	AGAATGTGCC	TGCCGTGTTG	GCTCCGTTGG	720
TGCGGACCCC	GTATATGATC	GCCGCCGTCA	TAGCCGACAC	CAGCGCGAGG	GCTACCAACA	780
TGCCGATCAG	CAGCCCGCTG	TGCCGTCGCT	TCGGGTAGGA	CACCTCGCGC	GGCACGCGCG	840
GATATCGGCG	GGGCGGCAGC	GCCGCGCTGT	CTGCCGCTCC	CGGGGCGAAG	GCCGGTTCGG	900
CGGCGCCGAG	CTCGTGGGGG	TAGTCCAGGG	CTTGGGGTTC	GTGGGTAGAG	GGCTCGGGGG	960
ACGGCGCCGG	TCCGTTGTGT	CCGACACCGG	GGTTCGCGGA	GTGGGAGACG	GGCATTTGGT	1020
TTCTCTTAGG	GTGGTGGACG	GGACCAGCTG	CTAGGGCGAC	AACCGCCCGT	CGCGTCAGCC	1080
GGCAGCATCG	GCAATCAGGT	GAGCTCCCTA	GGCAGGCTAG	CGCAACAGCT	GCCGTCAGCT	1140
CTCAACGCGA	CGGGGCGGCG	CGCGGCGCGC	ATAATGTGTA	AAGACTAGGC	AACCTTAGGA	1200
ACGAAGGACG	GAGATTTTGT	GACGATC				1227

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGGTGTCGG	CGGATCCCGC	GGGTGGTTGA	ACGGCAACGG	CGGGGCGCGC	GGGGCCGGCG	60
GGACCGGCGC	TAAACGGTGT	GCCGCGCGCA	ACGCTGGTT	GTTCCGGGCGC	GGCGGGTCCG	120
GCGGNGCCGG	CACCAATGTT	GGNGTCGGCG	GGTCCGCGCG	ATTGTCTTAC	GGCAACGGCG	180
G						181

(2) INFORMATION FOR SEQ ID NO:37:

10084913.022502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGGTGTCGG	CGGATCCGGC	GGGTGGTTGA	ACGGCAACGG	CGGTGTCGGC	GGCCGGGGCG	60
GCGACGGCGT	CTTTGCCCGT	GCCGGCGGCC	AGGGCGGCCT	CGGTGGGCAG	GGCGGCAATG	120
GCGGCGGCTC	CACCGGCGGC	AACGGCGGTC	TTGGCGGCGC	GGGCGGTGGC	GGAGGCAACG	180
CCCCGGACGG	CGGCTTCGGT	GGCAACGGCG	GTAAGGGTGG	CCAGGGCGGN	ATTGGCGGCG	240
GCACTCAGAG	CGCGACCGGC	CTCGNGGTG	ACGGCGGTGA	CGGCGGTGAC		290

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GATCCAGTGG	CATGGNGGGT	GTCA GTGGA	GCAT	34
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(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCGTGCTG	CGTCCCCCCC	TTGCCGCCGA	CGCCACCGGT	CCCACCGTTA	CCGAACAAGC	60
TGGCGTGGTC	GCCAGCACCC	CCGGCACCGC	CGACGCCGGA	GTCGAACAT	GGCACCGTCG	120
TATCCCCACC	ATTGCCGCGC	GNCCACCGG	CACCG			155

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGCGTTCA	CGGGGCGCCG	GGGACCGGGC	AGCCCGGNGG	GGCCGGGGGG	TGG	53
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(2) INFORMATION FOR SEQ ID NO:41:

10084843.022502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCCACCGC	GGGTGCAGAC	GGTGCCCGCG	GCGCCACCCC	GACCAGCGGC	GGCAACGGCG	60
GCACCGCGCG	CAACGGCGCG	AACGCCACCG	TCGTCGGNGG	GGCCGGCGGG	GCCGCGCGCA	120
AGGGCGGCAA	CG					132

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCGGCGCG	CGGNACGGNC	GGGGACGGCG	GCAAGGGCGG	NAACGGGGGC	GCCGNAGCCA	60
CCNGCCAAGA	ATCCTCCGNG	TCCNCCAATG	GCGCGAATGG	CGGACAGGGC	GGCAACGGCG	120
GCANCGGGCG	CA					132

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCACGAGG	ATCGGTACCC	CGCGGCATCG	GCAGCTGCCG	ATTGCGCGGG	TTTCCCCACC	60
CGAGGAAAGC	CGCTACCAGA	TGGCGCTGCC	GAAGTAGGGC	GATCGGTTCC	CGATGCCGCG	120
ATGAACGGCG	GGCATCAAAT	TAGTGACAGG	ACCTTTCAGT	TTAGCGACGA	TAATGGCTAT	180
AGCACTAAGG	AGGATGATCC	GATATGACGC	AGTCGCAGAC	CGTGACGGTG	GATCAGCAAG	240
AGATTTTGAA	CAGGGCCAAC	GAGGTGGAGG	CCCCGATGGC	GGACCCACCG	ACTGATGTCC	300
CCATCACACC	GTGCGAACTC	ACGGNGGNTA	AAAAAGCGCG	CCAACAGNTG	GTNTGTGTCC	360
CCGACAACAT	GCGGGAATAC	CTGGCGGCGG	GTGCCAAGA	GCGGCAGCGT	CTGGCGACCT	420
CGCTGCGCAA	CGCGGCCAAG	GNGTATGGCG	AGGTTGATGA	GGAGGCTGCG	ACCGCGCTGG	480
ACAACGACGG	CGAAGGAAC	GTGCAGGCGG	AATCGGCGCG	GGCGGTCGGA	GGGGACAGTT	540
CGGCGCAACT	AACGATACG	CCGAGGGTGG	CCACGCGCGG	TGAACCCAAC	TTTCATGGATC	600
TCAAAGAAGC	GGCAAGGAAG	CTCGAAACGG	GCGACCAAGG	CGCATCGCTC	GCGCACTGNG	660
GGGATGGGTG	GAACACTTNC	ACCTTGACGC	TGCAAGGCGA	CG		702

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

10084843.022502

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAAGCGCAG	CGTGTCGGG	CGACGTGGG	GTCAAAGCG	CATCGCTCG	TGGCGGTGGA	60
GGCGGCGGG	TGCCGTCGG	GCCGTGGGA	TCCGCGATG	GGGGCGCCGA	ATCGGTGCGG	120
CCCGCTGGG	CTGGTGACAT	TGCCGGCTTA	GGCCAGGGAA	GGGCGGCGG	CGCGGCGCGG	180
CTGGGCGCG	GTGGCATGG	AATGCGCAT	GGTGCCGCG	ATCAGGGACA	AGGGGGCGCC	240
AAGTCCAAG	GTTCTCAGCA	GGAAGACGAG	GCGCTCTACA	CCGAGGATCC	TCGTGCGG	298

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGCACGAG	ATCGAATCG	GTCGCCGGG	GCACAGCGT	GCACTGCACC	AGTGGAGGAG	60
CCATGACCTA	CTGCCCGGG	AACCCCGGAT	ACCCGCAAGC	GCAGCCCGCA	GGCTCTACG	120
GAGGCGTCAC	ACCCTCGTTC	GCCACGCGG	ATGAGGGTGC	GAGCAAGCTA	CCGATGTACC	180
TGAACATCG	GGTGGCAGTG	CTCGGTCTGG	CTGCGTACTT	CGCCAGCTTC	GGCCCAATGT	240
TCACCCTCAG	TACCGAACTC	GGGGGGGGTG	ATGGCGCAGT	GTCGGGTGAC	ACTGGGCTGC	300
CGGTCCGGGT	GGCTCTGCTG	GCTGCGCTGC	TTGCCGGGGT	GGTTCTGGTG	CCTAAGGCCA	360
AGAGCCATGT	GACGGTAGTT	GCGGTGCTCG	GGGTACTCGG	CGTATTTCTG	ATGGTCTCGG	420
CGACGTTTAA	CAAGCCCGAC	GCCTATTGGA	CCGGTTGGGC	ATTGTGGGTT	GTGTTGGCTT	480
TCATCGTGTT	CCAGGCGGTT	CGGCGAGTCC	TGGCGCTCTT	GGTGGAGACC	GGCGCTATCA	540
CCGCGCCGCG	GCCGCGGCCC	AAGTTCGACC	CGTATGGACA	GTACGGGCGG	TACGGGCAGT	600
ACGGGCGAGT	CGGGGTGACG	CCGGGTGGGT	ACTACGGTCA	CGAGGGTGCT	CAGCAGGCGG	660
CGGGACTGCA	GTCGCCCGGC	CGCAGCAGT	CTCCGCGAGC	TCCCAGATAT	GGGTCCGAGT	720
ACGGCGGCTA	TTCGTCAGT	CCGAGCCAAT	CGGGCAGTGG	ATACACTGCT	CAGCCCCCGG	780
CCGAGCGCCG	GGCGCAGTCC	GGGTGCAAC	AATCGCACCA	GGGCCCATCC	ACGCCACCTA	840
CCGGCTTCC	GAGCTTCAGC	CCACCACCAC	CGGTGAGTGC	CGGGACGGGG	TCCGAGGCTG	900
GTTCCGCTCC	AGTCAACTAT	TCAAACCCCA	CGGGGGGCGA	GCAGTCTGTC	TCCCCCGGGG	960
GGGCGCGGTT	CTAACCGGGC	GTTCCCGGCT	CCGGTCGCGC	GTGTGCGCGA	AGAGTGAACA	1020
GGGTGTGAGC	AAGCGCGGAC	GATCCTCGTG	CCGAATTC			1058

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGCACGAGA	GACCGATGCC	GCTACCCCTG	CGCAGGAGGC	AGGTAATTTT	GAGCGGATCT	60
CCGGCGACCT	GAAAAACCCAG	ATCGACCAGG	TGGAGTCGAC	GGCAGGTTCT	TTGCAGGGCC	120
AGTGCGCGGG	CGCGGCGGGG	ACGGCGCCCC	AGGCGCGGCT	GGTGCCTTTC	CAGAAGACAG	180
CCAATAAGCA	GAAGCAGGAA	CTCGACGAGA	TCTCGACGAA	TATTCGTGAG	GCCGCGCTCC	240
AATACTCGAG	GGCCGAGCAG	GAGCAGCAGC	AGGCGCTGTC	CTCGCAAATG	GGCTTCTGAC	300
CCGCTAATAC	GAAAAAAGAC	GGAGCAA				327

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGGTCGCGAT GATGGCGTTG TCGAACGTGA CCGATTCTGT ACCGCCGTCG TTGAGATCAA	60
CCAACAACGT GTTGGCGTCG GCAAATGTGC CGNACCGTG GATCTCGGTG ATCTTGTTCT	120
TCTTCATCAG GAAGTCACA CCGGCCACCC TGCCCTCGGN TACCTTCGG	170

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCCGGCGG CACGGGGGGT GCGGCGGCA GCACCGCTGG CGTGGCGGC AACGGCGGGG	60
CGGGGGGTGG CGGCGGAACC GGTGGGTGC TCTTCGGCAA CGCGGTGCC GGCGGCGCAG	120
GGGCCGT	127

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGCGGGCAAG GCGGCACCG CCGCAACGG GAGCGCGCG GCCGCGGCA ACGCGCGCAA	60
CGCGGGCTCC GGCCTCAACG G	81

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGGCT GGCGGGCTCC GGCCAGAAGG GCGGTAACGG AGGAGCTGCC GGATTGTTG	60
GCAACGGCGG GGCCGGNGGT GCCGGCGCGT CCAACCAAGC CGGTAACGGC GNGGCCGCGC	120
GAACAGGTGG TGCCGGTGGG CTGATCTGG	149

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(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGCACGAGA	TCACACCTAC	CGAGTGATCG	AGATCGTCGG	GACCTCGCCC	GACGGTGTGC	60
ACGCGGNAAT	CCAGGGCGGT	CTGGCCGAG	CTGCGCAGAC	CATGCGCGCG	CTGGACTGGT	120
TCGAAGTACA	GTCAATTCTGA	GGCCACCTGG	TCGACGGAGC	GGTCGCGCAC	TTCCAGGTGA	180
CTATGAAAGT	CGGCTTCCGC	CTGGAGGATT	CCTGAACCTT	CAAGCGCGGC	CGATAACTGA	240
GGTGATCAT	TAAGGACCTT	TTCCAGAAAC	TCCTGACGCG	CTCGAAACGC	GGTTCAGCCG	300
ACGGTGGCTC	CGCCGAGGCG	CTGCCTCAA	AATCCTGCG	ACAATTCTGC	GGCGG	355

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCACC	ATCACCATCA	CATGCATCAG	GTGGACCCCA	ACTTGACACG	TCGCAAGGGA	60
CGATTGGCGG	CACTGGCTAT	CGCGCGGATG	GCCAGCGCCA	GCCTGGTGAC	CGTTGGCGGTG	120
CCGCGGACCG	CCAACGCGGA	TCGGGAGCCA	GCGCCCCCGG	TACCCACAAC	GGCCGCCCTCG	180
CCGCGGTCGA	CGCTGTCAGC	GCCACCCGCA	CGGCGGACAC	CTGTTGCCCC	CCCACACCG	240
GCGCGCGCCA	ACACGCGCAA	TGCCAGCCCG	GGCGATCCCA	ACGCAGCAC	TCCGCGCGCC	300
GACCCGAACG	CACCGCGGCC	ACCTGTCAAT	GCCCCAAACG	CACCCCAACC	TGTCGGGATC	360
GACAACCCGG	TTGGAGGATT	CAGCTTCGCG	CTGCCTGCTG	GCTGGGTGGA	GTCTGACGCC	420
GCCCACTTCG	ACTACGGTTC	AGCACTCCTC	AGCAAAACCA	CCGGGGACCC	GCCATTTC	480
GGACAGCCCG	CGCCGGTGGC	CAATGACACC	CGTATCGTGC	TCGGCCGGCT	AGACCAAAAG	540
CTTTACGCCA	GCGCGGAAGC	CACCGACTCC	AAGGCCGCGG	CCCGGTTGGG	CTCGGACATG	600
GGTGAGTTCT	ATATGCCCTA	CCCGGGCAAC	CGGATCAACC	AGGAAACCGT	CTCGCTCGAC	660
GCCAACGGGG	TGCTGGGAAG	CGCGTCGTAT	TACGAAGTCA	AGTTTCAGCGA	TCCGAGTAA	720
CCGAACGGCC	AGATCTGGAC	GGGCGTAATC	GGCTCGCCCG	CGGCGAACGC	ACCGGACGCC	780
GGGCCCCCTC	AGCGCTGATT	TGTGGTATGG	CTCGGGACCG	CAAACAACCC	GGTGGACAAG	840
GGGCGCGCCA	AGGCCTGGC	CGAATCGATC	CGGCCTTTGG	TCGCCCCCGC	GCCGGCGCCG	900
GCACCGGCTC	CTGCAGAGCC	CGCTCCGCGC	CCGGCGCCCG	CCGGGGAAGT	CGCTCCTACC	960
CCGACGACAC	CGACACCGCA	GCGGACCTTA	CCGGCCTGA			999

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
 1 5 10 15
 Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
 20 25 30
 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
 35 40 45
 Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
 50 55 60
 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
 65 70 75 80
 Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
 85 90 95
 Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
 100 105 110
 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
 115 120 125
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
 130 135 140
 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
 145 150 155 160
 Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
 165 170 175
 Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
 180 185 190
 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
 195 200 205
 Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
 210 215 220
 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
 225 230 235 240
 Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
 245 250 255
 Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
 260 265 270
 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
 275 280 285
 Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro
 290 295 300
 Ala Glu Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
 305 310 315 320
 Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
 325 330

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Xaa Asn Tyr Gly Gln Val

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```

1          5          10          15
Val Ala Ala Leu
          20

```

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro-Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys
1 5 10 15
Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro
 1 5 10 15
 Ala

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Gln Thr Ser
 1 5 10 15

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Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Phe Ala Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Thr Gly Ser Leu Asn Gln Thr His Asn Arg Arg Ala Asn Glu Arg Lys
 1 5 10 15
 Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala
 20 25 30
 Ala Ala Ala Ile Gly Ala Ala Ala Gly Val Thr Ser Ile Met Ala
 35 40 45
 Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro
 50 55 60
 Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln
 65 70 75 80
 Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala
 85 90 95
 Asn Lys Gly Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg
 100 105 110
 Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro
 115 120 125
 Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Gly Ser Ala
 130 135 140
 Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr
 145 150 155 160
 Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala
 165 170 175
 Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Xaa
 180 185

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
 1 5 10 15
 Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser
 20 25 30
 Gly Val Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg
 35 40 45
 Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser

50	55	60
Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val		
65	70	75
Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val		80
	85	90
Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val		95
	100	105
Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu		110
	115	120
Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser		125
	130	135
Thr Gly Gly Pro		140
145		

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr		
1	5	10
Gly Pro Asp Arg Ser Ala Ser Leu Ser Ser Leu Val Arg His Arg Arg Gln		15
	20	25
Gln Arg Asp Ala Leu Cys Leu Ser Ser Thr Gln Ile Ser Arg Gln Ser		30
	35	40
Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn		45
	50	55
Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu		60
65	70	75
Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Glu		80
	85	90
Glu Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser		95
	100	105
Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp		110
	115	120
Gln Lys Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu		125
	130	135
Ser Ala Ala Thr Ser Ser Thr Pro Arg Glu Ala Pro Tyr Glu Leu Asn		140
145	150	155
Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln		160
	165	170
Ala Val Val Leu Xaa Val Tyr His Asn Ala Gly Gly Thr His Pro Thr		175
	180	185
Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile		190
	195	200
Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val		205
	210	215
Phe Pro Ile Val Ala Arg		220
225	230	

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(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1          5          10          15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20          25          30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35          40          45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50          55          60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65          70          75          80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85          90          95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100         105         110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115         120         125
Gly Pro Pro Ala
130

```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
1          5          10          15
Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Leu Ser Asn Pro Pro
20          25          30
Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
35          40          45
Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa
50          55          60
Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
65          70          75          80
Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
85          90          95
Ser Glu Arg Lys
100

```

(2) INFORMATION FOR SEQ ID NO:68:

205220.346+3001

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
1      5      10      15
Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
20      25      30
Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp
35      40      45
Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
50      55      60
Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu
65      70      75      80
Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Gln Arg
85      90      95
Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro
100     105     110
Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
115     120     125
Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg
130     135     140
His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Arg Leu Pro Val Arg
145     150     155     160
Asp Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly
1      5      10      15
Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg
20      25      30
Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr
35      40      45
Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Gln Val Pro
50      55      60
Arg Gly Arg Lys Glu Ala Val Ala Ala Val Ala Ala Ser Leu Arg
65      70      75      80
Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly
85      90      95
Gln Thr Asp Thr Ala Ala Ala Ile Leu Ala Gly Thr Ala Pro Ala Ala
100     105     110

```

Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr
 115 120 125
 Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Glu Tyr
 130 135 140
 Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val
 145 150 155 160
 Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu
 165 170 175
 Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu
 180 185 190
 His Arg Pro Gly Arg Ser Thr Arg Arg Leu Glu Pro Arg Thr Leu Pro
 195 200 205
 Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe
 210 215 220
 Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro
 225 230 235 240
 Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro
 245 250 255
 Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro
 260 265 270
 Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala
 275 280 285
 Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu
 290 295 300
 Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr
 305 310 315 320
 Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Glu Gly Gln
 325 330 335
 Val Ser Arg Gln Asn Pro Thr Gly
 340

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala
 1 5 10 15
 Leu Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Gln Asp Cys Val Glu
 20 25 30
 Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile
 35 40 45
 Ile Tyr Arg Gln Arg Arg Ala Glu Leu Arg Thr Ala Lys Ala Leu Leu
 50 55 60
 Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Val Thr Val Leu
 65 70 75 80
 Arg Glu Arg Tyr Leu Leu His Asp Glu Gln Gly Arg Pro Ala Glu Ser
 85 90 95
 Thr Gly Glu Leu Met Asp Arg Ser Ala Arg Cys Val Ala Ala Glu
 100 105 110

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```

Asp Gln Tyr Glu Pro Gly Ser Ser Arg Arg Trp Ala Glu Arg Phe Ala
      115      120      125
Thr Leu Leu Arg Asn Leu Glu Phe Leu Pro Asn Ser Pro Thr Leu Met
      130      135      140
Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys Phe Val Leu Pro
145      150      155      160
Ile Glu Asp Ser Leu Gln Ser Ile Phe Ala Thr Leu Gly Gln Ala Ala
      165      170      175
Glu Leu Gln Arg Ala Gly Gly Gly Thr Gly Tyr Ala Phe Ser His Leu
      180      185      190
Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly Thr Ala Ser Gly
      195      200      205
Pro Val Ser Phe Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser
      210      215      220
Met Gly Gly Arg Arg Arg Gly Ala Cys Met Ala Val Leu Asp Val Ser
225      230      235      240
His Pro Asp Ile Cys Asp Phe Val Thr Ala Lys Ala Glu Ser Pro Ser
      245      250      255
Glu Leu Pro His Phe Asn Leu Ser Val Gly Val Thr Asp Ala Phe Leu
      260      265      270
Arg Ala Val Glu Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr
      275      280      285
Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile
      290      295      300
Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp
305      310      315      320
Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala
      325      330      335
Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn
      340      345      350
Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp
      355      360      365
Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp
      370      375      380
Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala
385      390      395      400
Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu
      405      410      415
Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg
      420      425      430
Leu Ala Thr Arg Leu Met Arg Arg Ile Gln Gln Ala Ala His Thr Ala
      435      440      445
Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp
      450      455      460
Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser
465      470      475      480
Val Ala Pro Thr Gly
      485

```

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu
1           5           10           15
Ile Tyr Trp Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val
20           25           30
Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala
35           40           45
Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His
50           55           60
Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu
65           70           75           80
Gly Asn Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Glu Thr Pro
85           90           95
Thr Pro Thr Ala Ala Val Gln Pro Pro Val Leu Lys Glu Gly Asp
100          105          110
Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro
115          120          125
Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn
130          135          140
Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala
145          150          155          160
Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp
165          170          175
Cys Ala Pro Ser Asn Glu Thr Leu Val Lys Thr Phe Ser Pro Gly Glu
180          185          190
Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg
195          200          205
Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val
210          215          220
Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn
225          230          235          240
Gln Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln
245          250          255
Ala Pro Pro Pro Glu Ser Pro Ala Gln Gly Gly
260          265

```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val
1           5           10           15
Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala
20           25           30
Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr
35           40           45

```

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Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala
 50 55 60
 Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp
 65 70 75 80
 Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Glu
 85 90 95
 Gln

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala
 1 5 10 15
 Cys Gly Gly Gly Thr Asn Ser Ser Ser Gly Ala Gly Gly Thr Ser
 20 25 30
 Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser
 35 40 45
 Thr Ala Gln Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg
 50 55 60
 Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala
 65 70 75 80
 Gly Val Thr Gln Phe Leu Asn Asn Glu Thr Asp Phe Ala Gly Ser Asp
 85 90 95
 Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Glu Arg
 100 105 110
 Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro Ile Ala
 115 120 125
 Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro
 130 135 140
 Thr Thr Ala Lys Ile Phe Asn Gly Thr Ile Thr Val Trp Asn Asp Pro
 145 150 155 160
 Gln Ile Gln Ala Leu Asn Ser Gly Thr Asp Leu Pro Pro Thr Pro Ile
 165 170 175
 Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln
 180 185 190
 Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser
 195 200 205
 Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly
 210 215 220
 Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Glu
 225 230 235 240
 Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr
 245 250 255
 Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys
 260 265 270
 Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu
 275 280 285
 Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile

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```

      290              295              300
Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr
305              310              315              320
Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly
      325              330              335
Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe
      340              345              350
Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser
      355              360

```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Asp
1      5      10      15
Gln Thr His Gln Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val
20      25      30
Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro
35      40      45
Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser
50      55      60
Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg
65      70      75      80
Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro
85      90      95
Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg
100      105      110
Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp
115      120      125
Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val
130      135      140
Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg
145      150      155      160
Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly
165      170      175
Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala
180      185      190
Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val
195      200      205
Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg
210      215      220
Ala Gly Pro Gln Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro
225      230      235      240
Leu Pro Ala Arg Ala Gly Gln Gln Gln Pro Ser Ser Ala Gly Gly Arg
245      250      255
Arg Ala Gly Gly Ala Glu Arg Ala Asp Pro Gly Gln Arg Gly Arg His
260      265      270
His Gln Gly Gly His Asp Pro Gly Arg Gln Gly Ala Gln Arg Gly Thr

```

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275 280 285
 Ala Gly Val Ala His Ala Ala Gly Pro Arg Arg Ala Ala Val Arg
 290 295 300
 Asn Arg Pro Arg Arg
 305

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly
 1 5 10 15
 Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys
 20 25 30
 Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala
 35 40 45
 Ser Pro Leu Glu Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys
 50 55 60
 Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr
 65 70 75 80
 Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Gln Trp Asn Leu Ser
 85 90 95
 Pro Arg Ala Gln Pro Ser Cys Ala Val Thr Val Glu Ser His Thr His
 100 105 110
 Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Leu Val Gln
 115 120 125
 Glu Glu Gln Pro Ser Asp Met Thr Asn His Pro Arg Tyr Ser Pro Pro
 130 135 140
 Pro Gln Gln Pro Gly Thr Pro Gly Tyr Ala Gln Gly Gln Gln Thr
 145 150 155 160
 Tyr Ser Gln Gln Phe Asp Trp Arg Tyr Pro Pro Ser Pro Pro Gln
 165 170 175
 Pro Thr Gln Tyr Arg Gln Pro Tyr Glu Ala Leu Gly Gly Thr Arg Pro
 180 185 190
 Gly Leu Ile Pro Gly Val Ile Pro Thr Met Thr Pro Pro Pro Gly Met
 195 200 205
 Val Arg Gln Arg Pro Arg Ala Gly Met Leu Ala Ile Gly Ala Val Thr
 210 215 220
 Ile Ala Val Val Ser Ala Gly Ile Gly Gly Ala Ala Ser Leu Val
 225 230 235 240
 Gly Phe Asn Arg Ala Pro Ala Gly Pro Ser Gly Gly Pro Val Ala Ala
 245 250 255
 Ser Ala Ala Pro Ser Ile Pro Ala Ala Asn Met Pro Pro Gly Ser Val
 260 265 270
 Glu Gln Val Ala Ala Lys Val Val Pro Ser Val Val Met Leu Glu Thr
 275 280 285
 Asp Leu Gly Arg Gln Ser Glu Glu Gly Ser Gly Ile Ile Leu Ser Ala
 290 295 300
 Glu Gly Leu Ile Leu Thr Asn Asn His Val Ile Ala Ala Ala Lys

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(2) INFORMATION FOR SEQ ID NO:77:

(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

[illegible]

(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Val	Pro	Pro	Ala	Pro	Pro	Leu	Pro	Pro	Leu	Pro	Pro	Ser	Pro	Ile	Ser
1				5					10					15	

Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
 20 25 30
 Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro
 35 40 45
 Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
 50 55 60
 Ser Pro Pro Leu Pro
 65

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
 1 5 10 15
 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
 20 25 30
 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35 40 45
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285

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Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
 355

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ser Pro Lys Pro Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr
 1 5 10 15
 Ala Ser Asp Pro Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala
 20 25 30
 Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys
 35 40 45
 Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala
 50 55 60
 Asn Pro Leu Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly
 65 70 75 80
 Val Pro Phe Arg Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp
 85 90 95
 Asp Trp Ser Asn Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val
 100 105 110
 Leu Asp Pro Ala Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn
 115 120 125
 Leu Gln Ala Gln Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys
 130 135 140
 Ile Thr Gly Thr Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly
 145 150 155 160
 Ala Lys Ser Ala Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser
 165 170 175
 His His Leu Val Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln
 180 185 190
 Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp
 195 200 205

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
 1 5 10 15
 Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
 20 25 30
 His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
 35 40 45
 Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
 50 55 60
 Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
 65 70 75 80
 Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
 85 90 95
 Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
 100 105 110
 Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
 115 120 125
 Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
 130 135 140
 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
 145 150 155 160
 Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
 165 170 175
 Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
 180 185 190
 Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
 195 200 205
 Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
 210 215 220
 Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
 225 230 235 240
 Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
 245 250 255
 Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
 260 265 270
 Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys
 275 280 285

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr
 1 5 10 15
 Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp
 20 25 30
 Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg

```

      35              40              45
Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg
  50              55              60
Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro
  65              70              75              80
Arg Glu Ala Leu Ala Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp
      85              90              95
Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu
      100              105              110
Gly Glu Gln Phe Met Gln Trp Phe Leu Gln Glu Gln Ile Glu Glu Val
      115              120              125
Ala Leu Met Ala Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn
      130              135              140
Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro
      145              150              155              160
Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu
      165              170

```

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

Arg Ala Asp Glu Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser Ile
  1              5              10              15
Ala Ala Gly Leu Thr Ala Ala Ala Ile Gly Ala Ala Ala Ala Gly
      20              25              30
Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro
      35              40              45
Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa
      50              55              60
Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp
      65              70              75              80
Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Glu Gly Gly Ile
      85              90              95
Gly Gly Xaa Glu Gly Xaa Xaa Arg Arg Xaa Gln
      100              105

```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn
  1              5              10              15
Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr

```

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(2) INFORMATION FOR SEQ ID NO:85:

(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu
1 5 10 15
Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln
20 25 30

```

Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp
    35          40          45
Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe
    50          55          60
His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
    65          70          75          80
Ile Leu Glu Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro
    85          90          95
Pro Ala Ala Gly Gly Gly Ala
    100

```

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```

Val Gln Cys Arg Val Trp Leu Glu Ile Gln Trp Arg Gly Met Leu Gly
 1          5          10          15
Ala Asp Gln Ala Arg Ala Gly Gly Pro Ala Arg Ile Trp Arg Glu His
    20          25          30
Ser Met Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala
    35          40          45
Thr Lys Glu Gly Arg Gly Ile Val Met Arg Val Pro Leu Glu Gly Gly
    50          55          60
Gly Arg Leu Val Val Glu Leu Thr Pro Asp Glu Ala Ala Ala Leu Gly
    65          70          75          80
Asp Glu Leu Lys Gly Val Thr Ser
    85

```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
 1          5          10          15
Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
    20          25          30
Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
    35          40          45
Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
    50          55          60
Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
    65          70          75          80
Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser Gln Met Gly Phe

```

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85

90

95

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
1           5           10           15
Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
           20           25           30
Pro Ile Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln
           35           40           45
Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
           50           55           60
Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa
65           70           75           80
Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
           85           90           95
Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
           100          105          110
Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
           115          120          125
Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
130          135          140
Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr
145          150          155          160
Leu Thr Leu Gln Gly Asp
           165

```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

Arg Ala Glu Arg Met
1           5

```

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
1           5           10           15
Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
20           25           30
Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
35           40           45
Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
50           55           60
Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Met Phe
65           70           75           80
Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
85           90           95
Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
100          105          110
Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
115          120          125
Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
130          135          140
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
145          150          155          160
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
165          170          175
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
180          185          190
Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala
195          200          205
Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
210          215          220
Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
225          230          235          240
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
245          250          255
Arg Arg Asn Gly Gly Pro Ala
260

```

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala
1           5           10           15
Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly
20           25           30
Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly
35           40           45
Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr

```

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(2) INFORMATION FOR SEQ ID NO:93:

(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Gly Cys Gly Glu Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn
1 5 10 15
Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile
20 25

(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly
1 5 10 15

(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Gly Cys Gly Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala
1 5 10 15
Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
20 25

(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Gly Cys Gly Gly Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu
1 5 10 15
Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu
20 25

(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Gly Cys Gly Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr
1 5 10 15
Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
20 25

(A) LENGTH: 28 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Gly Cys Gly Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu
 1 5 10 15
 Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 20 25

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGAAGATGG TGAAATCGAT CGCCGCAGGT CTGACCGCCG CGGCTGCAAT CGGCGCCGCT 60
 GCGGCCGGTG TGACTTCGAT CATGGCTGGC GCGCCGGTGC TATACCAGAT GCAGCCGGTC 120
 GTCTTCGGCG CGCCTACTGCC GTTGGACCCG GCATCCGCCC CTGACGTCCT GACCGCCGCC 180
 CAGTTGACCA GCCTGCTCAA CAGCCTCGCC GATCCCAACG TGTCTTTTCG GAACAAGGGC 240
 AGTCTGGTCG AGGGCGGCAT CGGGGGCACC GAGGCGCGCA TCGCCGACCA CAAGCTGAAG 300
 AAGCCGCGCG AGCACGGGGA TCTGCCGCTG TCGTTCAGCG TGACGAACAT CCAGCCGGCG 360
 GCGCGCGGTT CGGCCACCGC CGACGTTTCC GTCTCGGGTC CGAAGCTCTC GTCGCGGGTC 420
 ACCGAGAACG TCACGTTCTG GAATCAAGGC GGCTGGATGC TGTACGCGC ATCGGCGGATG 480
 GAGTTGCTGC AGGCCGCAGG GAACTGA 507

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala
 1 5 10 15
 Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro
 20 25 30
 Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu
 35 40 45
 Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
 50 55 60
 Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly
 65 70 75 80
 Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg Ile Ala Asp
 85 90 95
 His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro Leu Ser Phe

	100		110		110
Ser Val Thr Asn Ile Gln Pro Ala Ala Gly Ser Ala Thr Ala Asp					
	115		120		125
Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Gln Asn Val					
	130		135		140
Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met					
	145		150		155
Glu Leu Leu Gln Ala Ala Gly Asn					160
	165				

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CGTGGCAATG TCGTTGACCG TCGGGGCCGG GGTGCCTCC GCAGATCCCG TGGACGCGGT	60
CATTAAACACC ACCTGCAATT ACGGGCAGGT AGTAGCTGCG CTCAACGCGA CGGATCCGGG	120
GGCTGCCGCA CAGTTCAACG CCTCACCGGT GCGCAGTCC TATTTGCGCA ATTTCTCTGC	180
CGCACCGCCA CCTCAGCGCG CTGCCATGGC CGCGCAATTG CAAGCTGTGC CGGGGGCGGC	240
ACAGTACATC GGCCTTGTGC AGTCGGTTGC CGGCTCTGCG AACAACTATT AAGCCCATGC	300
GGGCCCCATC CGCGACCGCC GCATCGTCGC CGGGGCTAGG CCAGATTGCC CGCTCTCTCA	360
ACGGGCGGCA TCCCGCGACC CGGCATCGTC GCCGGGGCTA GGCCAGATTG CCCCGTCTCT	420
CAACGGGGCG CATCTCGTGC CGAATTCCTG CAGCCCGGGG GATCCACTAG TTCTAGAGCG	480
GCCGCCACCG CGGTGGAGCT	500

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro	
1	5 10 15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala	
	20 25 30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser	
	35 40 45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro	
	50 55 60
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala	
	65 70 75 80
Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr	
	85 90 95

(2) INFORMATION FOR SEQ ID NO:103:

202502: 2484800T

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGACAGAGC	AGCAGTGGAA	TTTCGCGGGT	ATCGAGGCCG	CGGCAAGCGC	AATCCAGGGA	60
AATGTCACGT	CCATTTCATT	CCTCCTTGAC	GAGGGGAAGC	AGTCCCTGAC	CAAGCTCGCA	120
GCGGCCTGGG	GCGGTAGCGG	TTCGGAAGCG	TACC			154

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met	Thr	Glu	Gln	Gln	Trp	Asn	Phe	Ala	Gly	Ile	Glu	Ala	Ala	Ala	Ser
1				5					10			15			
Ala	Ile	Gln	Gly	Asn	Val	Thr	Ser	Ile	His	Ser	Leu	Leu	Asp	Glu	Gly
		20					25				30				
Lys	Gln	Ser	Leu	Thr	Lys	Leu	Ala	Ala	Ala	Trp	Gly	Gly	Ser	Gly	Ser
		35				40					45				
Glu	Ala	Tyr													
		50													

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CGGTCGCGCA	CTTCCAGGTG	ACTATGAAAG	TCGGCTTCG	NCTGGAGGAT	TCCTGAACCT	60
TCAAGCGCGG	CGGATAACTG	AGGTGCATCA	TTAAGCGACT	TTCCAGAAC	ATCCTGACGC	120
GCTCGAAACG	CGGCACAGCC	GACGGTGGCT	CCGNCGAGGC	GCTGNCTCCA	AAATCCCTGA	180
GACAATTCGN	CGGGGGCGCC	TACAAGGAAG	TCGGTGCTGA	ATTGNCNGNG	TATCTGGTGC	240
ACCTGTGTGG	TCTGNAGCCG	GACGAAGCGG	TGCTCGACCT	CG		282

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATCGTACCC GTGCGAGTGC TCGGGCCGTT TGAGGATGGA GTGCACGTGT CTTTCGTGAT	60
GGCATACCCA GAGATGTTGG CGGCGGCGGC TGACACCCTG CAGAGCATCG GTGCTACCAC	120
TGTGGCTAGC AATGCCGCTG CGGCGGCCCC GACGACTGGG GTGGTCCCCC CCGCTGCCGA	180
TGAGGTGTCG GCGCTGACTG CGGCGCACTT CGCCGCACAT GCGGCGATGT ATCAGTCCGT	240
GAGCGCTCGG GCTGTGCGGA TTCATGACCA GTTCGTGGCC ACCCTTGCCA GCAGCGCCAG	300
CTCGTATCGG GCCACTGAAG TCGCCAATGC GCGGGCGGCC AGCTAAGCCA GGAACAGTCG	360
GCACGAGAAA CCACGAGAAA TAGGGACACG TAATGGTGGA TTTCGGGGCG TTACCACCGG	420
AGATCAACTC CCGCAGGATG TACGCCGGCC CGGGTTCCGC CTCGCTGGTG GCCGCGGCTC	480
AGATGTGGGA CAGCGTGCGC AGTGACCTGT TTTCGGCCGC GTCGGCGTTT CAGTCGGTGG	540
TCTGGGGTCT GACGGTGGGG TCGTGGATAG GTTCGTCGGC GGGTCTGATG GTGGCGGCCG	600
CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA GGCCGAGCTG ACCGCCGCCC	660
AGGTCCGGGT TGCTGCGGCG GCCTACGAGA CGCGTATG GCTGACGGTG CCCCCCGG	720
TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC GACCAACCTC TTGGGGCAAA	780
ACACCCCGGC GATCGCGCTG AACGAGGCCG AATACGCGCA GATGTGGGCC CAAGACGCCG	840
CCCGATGTTT TGCTACGCC GCGCGGACGG CGACGGCGAC GCGGACGTTG CTGCCGTTTC	900
AGGAGGCGCC GGAGATGACC AGCGCGGGTG GGCTCCTCGA GCAGGCCGCC CGGCTCGAGG	960
AGGCCTCCGA CACCGCCGCG GCGAACCAGT TGATGAACAA TGTGCCCCAG GCCTGCAAC	1020
AGCTGGCCCA GCCACGACG GGCACCACGC CTTCTTCCAA GCTGGGTGGC CTGTGGAAGA	1080
CGGTCTCGCC GCATCGGTG CCGATCAGCA ACATGGTGTG GATGGCCAAC AACCACATGT	1140
CGATGACCAA CTCGGGTGTG TCGATGACCA ACACCTTGAG CTCGATGTTG AAGGGCTTTG	1200
CTCCGGCGGC GGCGCCCCAG GCGGTGCAAA CCGCGGCGCA AAACGGGGTC CGGGCGATGA	1260
GCTCGCTGGG CAGCTCGCTG GGTCTCTCGG GTCTGGGCGG TGGGTGGCC GCCAACTTGG	1320
GTCGGGCGGC CTCGGTCGTT TCGTTGTCGG TGCCGCGAGC CTGGGCCGCG GCCAACCAGG	1380
CAGTCACCCC GCGGCGCGCG GCGCTGCCGC TGACCAAGCT GACCAGCGCC GCGGAAAGAG	1440
GGCCCGGGCA GATGCTGGGC GGGCTGCCGG TGGGCAGAT GGGCGCCAGG GCCGGTGGTG	1500
GGCTCAGTGG TGTGCTGCGT GTTCCGCCGC GACCCATATG GATGCCGCAT TCTCCGGCGG	1560
CCGGCTAGGA GAGGGGGCGC AGACTGTCGT TATTTGACCA GTGATCGGCG GTCTCGGTGT	1620

TTCCGCGGCC GGCTATGACA ACAGTCAATG TGCATGACAA GTTACAGGTA TTAGGTCCAG 1680
 GTTCAACAAG GAGACAGGCA ACATGGCCTC ACGTTTATG ACGGATCCGC ACGCGATGCG 1740
 GGACATGGCG GGCCTTTTGG AGGTGCACGC CCAGACGGTG GAGGACGAGG CTGCGCGGAT 1800
 GTGGGCGTCC GCGCAAAACA TTTCGGTGC GGGCTGGAGT GGCATGGCCG AGGCACCTC 1860
 GCTAGACACC ATGGCCCAGA TGAATCAGGC GTTTCGCAAC ATCGTGAACA TGCTGCACGG 1920
 GGTGCGTGAC GGGCTGGTTC GCGACGCCAA CAACTACGAG CAGCAAGAGC AGGCCTCCCA 1980
 GCAGATCCTC AGCAGCTAAC GTCAGCCGCT GCAGCACAAT ACTTTTACAA CGGAAGGAGA 2040
 ACAGGTTTCA TGACCATCAA CTATCAATTC GGGGATGTGC ACGCTCACGG CGCCATGATC 2100
 CGCGCTCAGG CCGGGTGTCT GGAGGCCGAG CATCAGGCCA TCATTCTGTA TGTGTTGACC 2160
 GCGAGTGACT TTTGGGGGCG CGCCGGTTGG GCGGCTGCC AGGGGTTTAT TACCAGTTG 2220
 GGCCGTAAC TCCAGTGAT CTACGAGCAG GCCAACGCC ACGGGCAGAA GGTGCAGGCT 2280
 GCCGGCAACA ACATGGCGCA AACCGACAGC GCCGTCGGCT CCAGCTGGGC CTGACACCAG 2340
 GCCAAGGCCA GGGACGTGTT GTACGAGTGA AGTTCTCTGC GTGATCCTT GGGTGGCAGT 2400
 CTAAGTGGTC AGTGCTGGGG TGTGTTGGTT TTGCTGCTTG GCGGTTCTT CSGTGCTGTT 2460
 CAGTGCTGCT CGGCTCGGG TGAGGACCTC GAGGCCCAGG TAGCGCGTCT CTTGATCCA 2520
 TTCGTCGTGT TGTTCGGCGA GGACGGCTCC GACGAGGCG ATGATCGAGG CGCGGTCGGG 2580
 GAAGATGCCC ACGACGTCGG TTCGGCGTCG TACCTCTCGG TTGAGGCGTT CCTGGGGTT 2640
 GTTGACCAG ATTGCGCGC AGATCTGCTT GGGGAAGCGG GTGAACGCCA GCAGGTCGGT 2700
 GCGGCGGGT TCGAGGTGCT CGGCCACCG GGGGAGTTTG TCGGTCAGAG CGTCAGTAC 2760
 CCGATCATAT TGGCAACAA CTGATTGCGC GTCGGGCTGG TCGTAGATGG AGTGACGAG 2820
 GGTGCGCACC CACGGCCAGG AGGGCTTCGG GGTGGCTGCC ATCAGATTGG CTGCGTAGTG 2880
 GGTTCGCA GCGTGCCAGG CCGCTGCGGG CAGGGTGGCG CCGATCGCG CCACAGGCC 2940
 GGCGTGGGCG TCGTGGTGA CCAGCGCGAC CCGGACAGG CCGCGGCGA CCAGGTCGCG 3000
 GAAGAACGCC AGCCAGCCGG CCCCGTCCTC GCGGAGGGT ACCTGGATGC CCAGGATC 3058

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

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Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1           5           10           15

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Gln Met Trp
          20           25           30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35           40           45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50           55           60

Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65           70           75           80

Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala
          85           90           95

Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
          100          105          110

Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
          115          120          125

Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
          130          135          140

Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
          145          150          155          160

Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
          165          170          175

Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
          180          185          190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
          195          200          205

Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
          210          215          220

Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
          225          230          235          240

Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
          245          250          255

Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
          260          265          270

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Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
275 280 285

Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
290 295 300

Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
305 310 315 320

Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
325 330 335

Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
340 345 350

Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
355 360 365

Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
370 375 380

Pro His Ser Pro Ala Ala Gly
385 390

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GACGTCAGCA CCCGCCGTGC AGGCGTGGAG CGTGGTCGGT TTGATCTGCG GGTCAAGGTG	60
ACGTCCTCTCG GCGTGTCGCG GCGGTGGATG CAGACTCGAT GCCGCTCTTT AGTGCAACTA	120
ATTTCGTTGA AGTGCCTGCG AGGTATAGGA CTTACAGATT GGTAAATGTA GCGTTCACCC	180
CGTGTGGGGG TCGATTTGGC CGGACCAGTC GTCACCAACG CTGGCGGTGC GCGCCAGGCG	240
GGCGATCAGA TCGCTTGACT ACCAATCAAT CTTGAGCTCC CGGGCCGATG CTCGGGCTAA	300
ATGAGGAGGA GCACGCGTGT CTTTCACTGC GCAACCGGAG ATGTTGGCGG CCGCGGCTGG	360
CGAACTTCGT TCCCTGGGGG CAACGCTGAA GGCTAGCAAT GCCGCGCAG CCGTGCCGAC	420
GACTGGGGTG GTGCCCCCGG CTGCCGACGA GGTGTCGCTG CTGCTTGCCA CACAATTCGG	480
TACGCATGCG GCGACGTATC AGACGGCCAG CGCCAAGGCC GCGGTGATCC ATGAGCAGTT	540
TGTGACCACG CTGGCCACCA GCGCTAGTTC ATATGCGGAC ACCGAGGCCG CCAACGCTGT	600
GGTCACCGGC TAGCTGACCT GACGGTATTC GAGCGGAAGG ATTATCGAAG TGGTGGATT	660

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CGGGGCGTTA CCACCGGAGA TCAACTCCGC GAGGATGTAC GCCGCCCCGG GTTCGGCCTC 720
 GCTGGTGGCC GCCGCGAAGA TGTGGGACAG CGTGGCGAGT GACCTGTTTT CGGCCGCGTC 780
 GCGCTTTCAG TCGTGGTCT GGGGTCTGAC GGTGGGGTCG TGGATAGGTT CGTCGGCGGG 840
 TCTGATGGCG GCGGCGGCCT CGCCGTATGT GCGTGGATG AGCGTCACCG CGGGGCAGGC 900
 CCAGCTGACC GCCGCCCAGG TCCGGGTTGC TCGGCGGCC TACGAGACAG CGTATAGGCT 960
 GACCGTGCCC CCGCCGGTGA TCGCCGAGAA CCGTACCAG CTGATGACGC TGACCGCGAC 1020
 CAACCTCTTG GGGCAAACA CGCCGGCGAT CGAGGCCAAT CAGGCCGCAT ACAGCCAGAT 1080
 GTGGGGCCAA GACGCGGAGG CGATGTATGG CTACGCCGCC ACGGCGGCGA CGGCACCGA 1140
 GCGGTGCTG CGTTCGAGG ACGCCCACT GATCACCAAC CCCGCGCGGC TCCTTGAGCA 1200
 GGCCGTCGCG GTCGAGGAGG CCATCGACAC CGCCGCGGCG AACCAGTTGA TGAACAATGT 1260
 GCCCCAAGCG CTGCAACAGC TGGCCCGAGC AGCGCAGGGC GTCGTACCTT CTTCCAAGCT 1320
 GGGTGGGCTG TGGACGGCGG TCTCGCCGCA TCTGTCCGCG CTCAGCAACG TCAGTTGAT 1380
 AGCCAACAAC CACATGTGCA TGATGGGCAC GGTGTGTGTC ATGACCAACA CTTGCACTC 1440
 GATGTTGAAG GGCTTAGCTC CGGCGGCGGC TCAGGCCGTG GAAACCGCG CGGAAAACGG 1500
 GGTCTGGGCG ATGAGCTCGC TGGCAGCCA GCTGGGTCG TCGTGGGTT CTTGCGGTCT 1560
 GGGCGCTGGG GTGGCCGCCA ACTTGGGTCG GGCGGCTCG GTGCGTTGCT TGTGCGTGCC 1620
 GCCAGCATGG GCCGCGGCCA ACCAGGCGGT CACCCGCGG GCGCGGGCGC TGCCGCTGAC 1680
 CAGCCTGACC AGCGCCGCCC AAACGCCCC CGGACACATG CTGGG 1725

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
 20 25 30
 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45

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Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 Leu Met Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Arg Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110
 Glu Asn Arg Thr Glu Leu Met Thr Leu Thr Ala Thr Asn Leu Leu Gly
 115 120 125
 Gln Asn Thr Pro Ala Ile Glu Ala Asn Gln Ala Ala Tyr Ser Gln Met
 130 135 140
 Trp Gly Gln Asp Ala Glu Ala Met Tyr Gly Tyr Ala Ala Thr Ala Ala
 145 150 155 160
 Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr
 165 170 175
 Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 Gln Gln Leu Ala Gln Pro Ala Gln Gly Val Val Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Thr Ala Val Ser Pro His Leu Ser Pro Leu Ser Asn
 225 230 235 240
 Val Ser Ser Ile Ala Asn Asn His Met Ser Met Met Gly Thr Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu His Ser Met Leu Lys Gly Leu Ala Pro Ala
 260 265 270
 Ala Ala Gln Ala Val Glu Thr Ala Ala Glu Asn Gly Val Trp Ala Met
 275 280 285
 Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu
 290 295 300
 Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser
 305 310 315 320
 Leu Ser Val Pro Pro Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro
 325 330 335

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Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr
 340 345 350

Ala Pro Gly His Met Leu Gly
 355

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AGTTCAGTCG AGAATGATAC TGACGGGCTG TATCCACGAT GGCTGAGACA ACCGAACCA	60
CGTCGGACGC GGGGACATCG CAAGCCGACG CGATGGCGTT GGCCGCCGAA GCCGAAGCCG	120
CCGAAGCCGA AGCGCTGGCC GCCCGGCGC GGGCCCGTGC CGTGCCGCC CGGTGAAGC	180
GTGAGGCGCT GGCATGGCC CCAGCCGAGG ACGAGAACGT CCCCAGGAT ATGCAGACTG	240
GGAAGACGCC GAAGACTATG ACGACTATGA CGACTATGAG GCCGCAGACC AGGAGGCCGC	300
ACGGTCGGCA TCCTGGCGAC GCGCGTTGCG GGTGCGGTTA CCAAGACTGT CCACGATTGC	360
CATGGCGGCC GCAGTCGTCA TCACTGCGG CTTACCCGG CTCAGCGGAT ACATTGTGTG	420
GCAACACCAT GAGGCCACCG AACGCCAGCA GCGCGCCGCG GCGTTCGCCG CCGGAGCCAA	480
GCAAGGTGTC ATCAACATGA CCTCGCTGGA CTTCAACAAG GCCAAGAAG ACGTCGCGCG	540
TGTGATCGAC AGCTCCACCG GCGAATTCAG GGATGACTTC CAGCAGCGGG CAGCCGATTT	600
CACCAAGGTT GTCGAACAGT CCAAAGTGGT CACCGAAGGC ACGGTGAACG CGACAGCCGT	660
CGAATCCATG AACGAGCATT CCGCCGTGGT GCTCGTCGCG GCGACTTCAC GGGTCACCAA	720
TTCCGCTGGG GCGAAGACG AACCACGTGC GTGGCGGCTC AAAGTGACCG TGACCGAAGA	780
GGGGGGACAG TACAAGATGT CGAAAGTTGA GTTCGTACCG TGACCGATGA CGTACGCGAC	840
GTCAACACCG AAACCACTGA GCACCAGAA GTCGCTGAGA TCGACTCAGC CGCAGGCGAA	900
GCCGGTGATT CGGCGACCGA GGCATTTGAC ACCGACTCTG CAACGGAATC TACCGCGCAG	960
AAGGGTCAGC GGCACCGTGA CTTGTGGCGA ATGCAGGTTA CTTTGAAGCC CGTTCGGSTG	1020
ATTCTCATCC TGCTCATGTT GATCTCTGGG GCGCGACGG GATGGCTATA CCTTGAGCAA	1080
TACGACCCGA TCAGCAGACG GACTCCGGCG CCGCCCGTGC TGCCGTCGCC GCGGCGTCTG	1140
ACGGGACAAT CGCGCTGTTG TGTATTCACC CGACACGTCG ACCAAGACTT CGTACCGCC	1200

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AGGTCGCACC TCGCCGGCGA TTTCCTGTCC TATACGACCA GTTCACGCAG CAGATCGTGG 1260
 CTCGCGCGGC CAAACAGAAG TCACTGAAAA CCACCGCCAA GGTGGTGCGC GCGGCCGTGT 1320
 CGGAGCTACA TCCGATTTCG GCCGTCGTTT TGGTTTITGT CGACCAGAGC ACTACCAGTA 1380
 AGGACAGCCC CAATCCGTCG ATGGCGGCCA GCAGCGTGAT GGTGACCCTA GCCAAGGTCTG 1440
 ACGGCAATTG GCTGATCACC AAGTTCACCC CGGTTTAGGT TGCCGTAGGC GGTCCGCAAG 1500
 TCTGACGGGG GCGCGGGTGG CTGCTCGTGC GAGATACCGG CCGTTCCTCC GACAATCAGC 1560
 GCGCCGACCTC AAACAGATCT CGGCCGCTGT CTAATCGGCC GGGTTATTTA AGATTAGTTG 1620
 CCACTGTATT TACCTGATGT TCAGATTGTT CAGCTGGATT TAGCTTCGCG GCAGGGCGGC 1680
 TGGTGCACTT TGCATCTGGG GTTGTGACTA CTTGAGAGAA TTTGACCTGT TGCCGACGTT 1740
 GTTTGCTGTC CATCATTTGT GCTAGTTATG GCCGAGCGGA AGGATTATCG AAGTGGTGGA 1800
 CTTCCGGGGC TTACCACCGG AGATCAACTC CGCGAGGATG TACCCCGGCC CGGGTTCCGGC 1860
 CTCGCTGGTG GCCCGCGCGA AGATGTGGGA CAGCGTGCGC AGTGACCTGT TTTCGCCCGC 1920
 GTCGCGGTTT CAGTCGGTGG TCTGGGGTCT GACGACGGGA TCGTGGATAG GTTCGTCGGC 1980
 GGGTCTGATG GTGGCGCGCG CCTCGCCGTA TGTGCGGTGG ATGAGCGTCA CCGCGGGGCA 2040
 GGCCGAGCTG ACCGCGCCCC AGGTCGGGGT TGCTGCGCGC GCCTACGAGA CGCGGTATGG 2100
 GCTGACGGTG CCCCCGCGG TGATCGCCGA GAACCGTGCT GAACCTGATGA TTCTGATAGC 2160
 GACCAACCTC TTGGGGCAAA ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGGGA 2220
 GATGTGGGCC CAAGACGCCG CCGGATGTTT TGGCTACGCC GCCACGGCGG CGACGGCGAC 2280
 CGAGGCGTTG CTGCCGTTTC AGGACGCCCC ACTGATCACC AACCCCGGCG GGCTCCTTGA 2340
 GCAGGCCGTC GCGGTCGAGG AGGCCATCGA CACCGCCGCG GCGAACCAGT TGATGAACAA 2400
 TGTGCCCAA GCGCTGCAAC AACTGGCCCA GCCACGAAA AGCATCTGCG CGTTCGACCA 2460
 ACTGAGTGAA CTCTGGAAG CCATCTCGCC GCATCTGTCG CCGCTCAGCA ACATCGTGTC 2520
 GATGCTCAAC AACCACGTGT CGATGACCAA CTCGGGTGTG TCGATGGCCA GCACCTTGCA 2580
 CTCAATGTTG AAGGGCTTTG CTCGCGCGGC GGCTCAGGCC GTGGAACCG CGCGCAAAA 2640
 CGGGGTCGAG GCGATGAGCT CGGTGGGCG CAGCTGGGT TCGTCTGCTG GTTCTTCGGG 2700
 TCTGGCGCT GGGGTGGCG CCAACTTGGG TCGGGCGGCC TCGGTCGGTT CGTTGTCGGT 2760
 GCCGCAGGCC TGGGCGCGG CCAACCAGGC GGTCACCCCG CGGCGCGGG CGCTGCCGCT 2820

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GACCAGCCTG ACCAGCGCCG CCCAAACCGC CCCCGGACAC ATGCTGGGCG GGCTACCGCT 2880
 GGGGCAACTG ACCAATAGCG GCGCGGGGTT CGGCGGGGTT AGCAATGCGT TCGGATGCC 2940
 GCCGCGGGCG TACGTAATGC CCCGTGTGCC CGCCGCGGG TAACGCCGAT CGGCACGCAA 3000
 TCGGGGCCCT CTATGCGGGC AGCGATC 3027

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Lys Met Trp
 20 25 30
 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45
 Val Val Trp Gly Leu Thr Thr Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110
 Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125
 Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
 130 135 140
 Trp Ala Gln Asp Ala Ala Met Phe Gly Tyr Ala Ala Thr Ala Ala
 145 150 155 160
 Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr
 165 170 175
 Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu

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195 200 205

Gln Gln Leu Ala Gln Pro Thr Lys Ser Ile Trp Pro Phe Asp Gln Leu
210 215 220

Ser Glu Leu Trp Lys Ala Ile Ser Pro His Leu Ser Pro Leu Ser Asn
225 230 235 240

Ile Val Ser Met Leu Asn Asn His Val Ser Met Thr Asn Ser Gly Val
245 250 255

Ser Met Ala Ser Thr Leu His Ser Met Leu Lys Gly Phe Ala Pro Ala
260 265 270

Ala Ala Gln Ala Val Glu Thr Ala Ala Gln Asn Gly Val Gln Ala Met
275 280 285

Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu
290 295 300

Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser
305 310 315 320

Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro
325 330 335

Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr
340 345 350

Ala Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn
355 360 365

Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro
370 375 380

Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly
385 390 395

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATCGGAGGG AGTGATCACC ATGCTGTGGC ACGCAATGCC ACCGGAGTAA ATACCCGACG	60
GCTGATGGCC GGC GCGGGT CGGCTCCAAT GCTTGCGGCG GCCGCGGGAT GGCAGACGCT	120
TTCCGGCGCT CTGGACGCTC AGGCCGTGCA GTTGACCGCG CGCCTGAACCT CTCTGGGAGA	180
AGCCTGGACT GGAGGTGGCA GCGACAAGGC GCTTGCGGCT GCAACGCCGA TGGTGGTCTG	240

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GCTACAAACC GCGTCAACAC AGGCCAAGAC CCGTGCATG CAGGCGACGG CGCAAGCCGC 300
 GGCATACACC CAGGCCATGG CCACGACGCC GTCGCTGCCG GAGATCGCCG CCAACACAT 360
 CACCCAGGCC GTCCTTACGG CCACCAACTT CTTCCGTATC AACACGATC CGATCGCGTT 420
 GACCGAGATG GATTATTTC A TCCGTATGTG GAACGAGGCA GCCCTGGCAA TGGAGSTCTA 480
 CCAGGCCGAG ACCGCGGTTA ACACGCTTTT CGAGAAGCTC GAGCCGATGG CGTCGATCCT 540
 TGATCCCGGC GCGAGCCAGA GCACGACGAA CCCGATCTTC GGAATGCCCT CCCCTGGCAG 600
 CTCAACACCG GTTGGCCAGT TGCCGCCGGC GGCTACCCAG ACCCTCGGCC AACTGGGTGA 660
 GATGAGCGGC CCGATGCAGC AGCTGACCCA GCCGCTCGAG CAGGTGACGT CGTTGTTCAG 720
 CCAGGTGGGC GGCACCGCGC GCGGCAACCC AGCCGACGAG GAAGCCGCGC AGATGGGCCT 780
 GCTCGGCACC AGTCCGCTGT CGAACCATCC GCTGGCTGGT GGATCAGGCC CCAGCGCGGG 840
 CGCGGGCCTG CTGCGCGCGG AGTCGCTACC TGGCGCAGGT GGGTCGTTGA CCCGCACGCC 900
 GCTGATGTCT CAGCTGATGC AAAAGCCGGT TGCCCCCTCG GTGATGCCGG CGGCTGCTGC 960
 CGGATCGTCG GCGACGGGTG GCGCCGCTCC GGTGGGTGCG GGAGCGATGG GCCAGGTTGC 1020
 GCAATCCGGC GGTCCACCA GCGCCGGTCT GGTGCGCGCG GCACCGCTCG CGCAGGAGCG 1080
 TGAAGAAGAC GACGAGGAGC ACTGGGACGA AGAGGACGAC TGGTGAGCTC CCGTAATGAC 1140
 AACAGACTTC CCGGCCACCC GGGCCGGAAG ACTTGCCAAC AITTTGGCGA GGAAGGTAAA 1200
 GAGAGAAAGT AGTCCAGCAT GGCAGAGATG AAGACCGATG CCGTACCCT CGCGCAGGAG 1260
 GCAGGTAATT TCGAGCGGAT CTCGCGCGAC CTGAAAACCC AGATCGACCA GGTGGAGTCG 1320
 ACGGCAGGTT CGTTGCAGGG CCACTGGCGC GCGCGCGCGG GGACGGCCGC CCAGGCCGCG 1380
 GTGGTGCGCT TCCAAGAAGC AGCCAATAAG CAGAAGCAGG AACTCGACGA GATCTCGACG 1440
 AATATTCGTC AGGCCGCGCT CCAATACTCG AGGGCCGACG AGGAGCAGCA GCAGGCGCTG 1500
 TCCTCGCAA TGGGCTTCTG ACCCGCTAAT ACGAAAAGAA ACGGAGCAAA AACATGACAG 1560
 AGCAGCAGTG GAATTCGCG GGTATCGAGG CCGCGGCAAG CGCAATCCAG GGAAT 1616

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTAGTGGATG GGACCATGGC CATTTTCTGC AGTCTCACTG CCTTCTGTGT TGACATTTTG	60
GCACGCCGGC GGAAACGAAG CACTGGGGTC GAAGAACGGC TCGCTGCCA TATCGCCGG	120
AGCTTCCATA CCTTCGTGCG GCCGGAAGAG CTGTGCTAG TCGCCGCCA TGACAACCTC	180
TCAGAGTGCG CTCAAACGTA TAAACACGAG AAAGGGCGAG ACCGACGGAA GGTGGAATCT	240
GCCCGATCCC GTGTTTCGCT ATTCTACGCG AACTCGGCGT TGCCCTATGC GAACATCCCA	300
GTGACGTTGC CTTCGGTCGA AGCCATTGCC TGACCGGCTT CGCTGATCGT CCGCGCCAGG	360
TTCGACGCG CGTTGTTTCAG CTCGGTAGCC GTGGCGTCCC ATTTTGTCTG GACACCTCG	420
TACGCCTCCG AA	432

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met	Leu	Trp	His	Ala	Met	Pro	Pro	Glu	Xaa	Asn	Thr	Ala	Arg	Leu	Met	1	5	10	15
Ala	Gly	Ala	Gly	Pro	Ala	Pro	Met	Leu	Ala	Ala	Ala	Ala	Gly	Trp	Gln	20	25	30	
Thr	Leu	Ser	Ala	Ala	Leu	Asp	Ala	Gln	Ala	Val	Glu	Leu	Thr	Ala	Arg	35	40	45	
Leu	Asn	Ser	Leu	Gly	Glu	Ala	Trp	Thr	Gly	Gly	Gly	Ser	Asp	Lys	Ala	50	55	60	
Leu	Ala	Ala	Ala	Thr	Pro	Met	Val	Val	Trp	Leu	Gln	Thr	Ala	Ser	Thr	65	70	75	80
Gln	Ala	Lys	Thr	Arg	Ala	Met	Gln	Ala	Thr	Ala	Gln	Ala	Ala	Ala	Tyr	85	90	95	
Thr	Gln	Ala	Met	Ala	Thr	Thr	Pro	Ser	Leu	Pro	Glu	Ile	Ala	Ala	Asn	100	105	110	
His	Ile	Thr	Gln	Ala	Val	Leu	Thr	Ala	Thr	Asn	Phe	Phe	Gly	Ile	Asn	115	120	125	
Thr	Ile	Pro	Ile	Ala	Leu	Thr	Glu	Met	Asp	Tyr	Phe	Ile	Arg	Met	Trp	130	135	140	

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Asn Gln Ala Ala Leu Ala Met Glu Val Tyr Gln Ala Glu Thr Ala Val
 145 150 155 160
 Asn Thr Leu Phe Glu Lys Leu Glu Pro Met Ala Ser Ile Leu Asp Pro
 165 170 175
 Gly Ala Ser Gln Ser Thr Thr Asn Pro Ile Phe Gly Met Pro Ser Pro
 180 185 190
 Gly Ser Ser Thr Pro Val Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr
 195 200 205
 Leu Gly Gln Leu Gly Glu Met Ser Gly Pro Met Gln Gln Leu Thr Gln
 210 215 220
 Pro Leu Gln Gln Val Thr Ser Leu Phe Ser Gln Val Gly Gly Thr Gly
 225 230 235 240
 Gly Gly Asn Pro Ala Asp Glu Glu Ala Ala Gln Met Gly Leu Leu Gly
 245 250 255
 Thr Ser Pro Leu Ser Asn His Pro Leu Ala Gly Ser Gly Pro Ser
 260 265 270
 Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly
 275 280 285
 Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val
 290 295 300
 Ala Pro Ser Val Met Pro Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly
 305 310 315 320
 Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser
 325 330 335
 Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln
 340 345 350
 Glu Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp
 355 360 365

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
 1 5 10 15

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Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
 20 25 30
 Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
 35 40 45
 Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
 50 55 60
 Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly
 65 70 75 80
 Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser
 85 90 95
 Gln Met Gly Phe
 100

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GATCTCCGGC GACCTGAAAA CCCAGATCGA CCAGGTGGAG TCGACGGCAG GTTCGTTGCA	60
GGGCCAGTGG CGCGGCGCGG CGGGGACGGC CGCCCAGGCC GCGGTGGTGC GCTTCCAAGA	120
AGCAGCCAAT AAGCAGAAGC AGGAACCTGA CGAGATCTCG ACGAATATTG GTCAGGCCGG	180
CGTCCAATAC TCGAGGGCCG ACGAGGAGCA GCAGCAGGCG CTGTCTCTCG AAATGGGCTT	240
CTGACCCGCT AATACGAAAA GAAACGGAGC AAAAACATGA CAGAGCAGCA GTGGAATTTT	300
GCGGGTATCG AGGCCGCGGC AAGCGCAATC CAGGGAAATG TCACGTCCAT TCATTCCCTC	360
CTTGACGAGG GGAAGCAGTC CCTGACCAAG CTCGCA	396

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala	
1 5 10 15	

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Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln
 20 25 30
 Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu
 35 40 45
 Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser
 50 55 60
 Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GTGGATCCCG ATCCCGTGT TCGCTATTCT ACGCGAACTC GCGCTTGCCC TATGCGAACA 60
 TCCAGTGCAC GTTGCCCTCG GTCGAAGCCA TTGCTGACCC GGCCTCGCTG ATCGTCGCGC 120
 CCAGGTTCTG CAGCGCGTTG TTCAGCTCGG TAGCCGTGGC GTCCCATTTT TGCTGGACAC 180
 CCTGTACGCG CTCCGAACCG CTACCGCCCC AGGCCGCTGC GAGCTTGTCG AGGGACTGCT 240
 TCCCTCGTGC AAGGAGGGAA TGAATGGACG TGACATTGCC CTGGATTGCG CTGCGCGCGG 300
 CCTCGATACC CGCGAAATTC CACTGCTGCT CTGTCATGTT TTGCTCCGT TTCITTTGCT 360
 ATTAGCGGGT CAGAAGCCCA TTGCGA 387

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CGGCACGAGG ATCTCGGTTG GCCCAACGGC GCTGGCGAGG GCTCCGTGCC GGGGCGGAGC 60
 TGCGCGCCGG ATGCTTCCTC TGCCCGCAGC CGCGCTGGA TGGATGGACC AGTTGCTACC 120
 TTCCCGACGT TTCGTTCCGT GTCTGTGCGA TAGCGGTGAC CCCGCGCGCG ACGTCGGGAG 180
 TGTGGGGGGG CAGGCCGGGT CGGTGTTTCG GCCGGGGAGC CAGACGGTCT GGACGGAACG 240

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GGCGGGGGTT CGCCGATTGG CATCTTTGCC CA

272

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val
 1 5 10 15

Val Ala Ala Leu
 20

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys
 1 5 10 15

Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
1 5 10 15

Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn
20 25 30

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Asp Pro Pro Asp Pro His Gln Xaa Asp Met Thr Lys Gly Tyr Tyr Pro
1 5 10 15

Gly Gly Arg Arg Xaa Phe
20

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Pro Gly Tyr Thr Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Xaa Xaa Gly Phe Thr Gly Pro Gln Phe Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Third Residue Can Be Either a Gln or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Xaa Pro Xaa Val Thr Ala Tyr Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Xaa Xaa Xaa Glu Lys Pro Phe Leu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Xaa Asp Ser Glu Lys Ser Ala Thr Ile Lys Val Thr Asp Ala Ser
1 5 10 15

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(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Ala	Gly	Asp	Thr	Xaa	Ile	Tyr	Ile	Val	Gly	Asn	Leu	Thr	Ala	Asp
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Ala	Pro	Glu	Ser	Gly	Ala	Gly	Leu	Gly	Gly	Thr	Val	Gln	Ala	Gly
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Xaa	Tyr	Ile	Ala	Tyr	Xaa	Thr	Thr	Ala	Gly	Ile	Val	Pro	Gly	Lys	Ile
1				5					10					15	

Asn	Val	His	Leu	Val
			20	

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

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GCAACGCTGT CGTGGCCITT GCGGTGATCG GTTTCGCCCTC GCTGGCGGTG GCGGTGGCGG 60
 TCACCATCCG ACCGACCGCG GCCTCAAAAC CGGTAGAGGG ACACCAAAAC GCCCAGCCAG 120
 GGAAGTTTCAT GCCGTTGTTG CCGACGCAAC AGCAGGCGCC GGTCCCGCCG CCTCCGCCCG 180
 ATGATCCCAC CGCTGGATT CAGGGCGGCA CCATTCCGGC TGTACAGAAC GTGTGCGCGC 240
 GGCCGGGTAC CTCACCCGGG GTGGGTGGGA CGCGGCTTC GCCTGCGCCG GAAGCGCCGG 300
 CCGTGCCCGG TGTGTGCCT GCCCCGGTGC CAATCCCGGT CCCGATCATC ATTCCCCCGT 360
 TCCCGGGTGT GCAGCCTGGA ATGCCGACCA TCCCCACCGC ACCGCGACG ACGCCGGTGA 420
 CCACGTCGGC GACGACGCCG CCGACCACGC CGCCGACCAC GCCGGTGACC ACGCCGCCAA 480
 CGACGCCGCC GACCACGCCG GTGACCACGC CGCCAACGAC GCCGCGGACC ACGCCGGTGA 540
 CCACGCCACC AACGACCGTC GCCCCGACGA CCGTCGCCCC GACGACGGTC GCTCCGACCA 600
 CCGTCGCCCC GACCACGGTC GCTCCAGCCA CGGCCACGCC GACGACCGTC GCTCCGCAGC 660
 CGACGCAGCA GCCCACGCAA CAACCAACCC AACAGATGCC AACCCAGCAG CAGACCGTGG 720
 CCCCAGACAG GGTGGCGCCG GCTCCGCAGC CGCGTCCGG TGCCCGCAAC GGCAGCGGCG 780
 GGGGCGACTT ATTCGGCGGG TTCTGATCAC GGTGCGCGGT TCACTACGGT CGGAGGACAT 840
 GGCCGGTGAT GCGGTGACGG TGTGTGCTGCC CTGTCTCAAC GA 882

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CCATCAACCA ACCGCTCGCG CCGCCGCGC CGCCGATCC GCCGTGCGCG CCACGCCCGC 60
 CGGTGCCTCC GGTGCCCCCG TTGCGCCGT CGCGCGCGTC GCGCGGACC GGTGGGTGC 120
 CTAGGGCGCT GTTACCGCCC TGGTTGGCGG GGACGCGCC GGCACCACCG GTACCGCCGA 180
 TGGCGCGGTT GCCCGCGGCG GCACCGTTGC CACCGTTGCC ACGTTGCCA CCGTTGCCGA 240
 CCAGCCACCC GCCCGGACCA CCGGCACCGC CGGCGCGGCC CGCACGCGCG GCGTGCCCGT 300
 TCGTGCCCGT ACCGCCGGCA CCGCGGTTGC CGCGGTCACC GCCGACGGAA CTACCGCGCG 360
 ACGCGGCGTG CCCGCGGCG CCGCCCGCAC CGCCATTGGC ACGCGGTC ACGCGGCGTG 420

GGAGTGCCGC GATTAGGGCA CTGACCGGCG CAACCAGCGC AAGTACTCTC GGTACCCGAG	480
CACTTCCAGA CGACACCACA GCACGGGGTT GTCGGCGGAC TGGGTGAAAT GGCACCCGAT	540
AGCGGCTAGC TGTGGCTGC GGTCAACCTC GATCATGATG TCGAGGTGAC CGTGACCGCG	600
CCCCCGAAG GAGGCGCTGA ACTCGGCGTT GAGCCGATCG GCGATCGGTT GGGCAGTGC	660
CCAGGCCAAT ACGGGGATAC CGGGTGTCTA AGCCGCCGCG AGCGCAGCTT CGGTTCGCGG	720
ACNGTGGTCG GGGTGGCCTG TTACGCCGTT GTNCTCGAAC ACGAGTAGCA GGTCTGCTCC	780
GGCGAGGGCA TCCACCACGC GTTGCGTCAG CTCGT	815

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAGCCGCC GGCTGAGGTC TCAGATCAGA GAGTCTCCGG ACTACCCGGG GCGGTTTCAGC	60
CTTCTCCAG AACAACTGCT GAAGATCCTC GCCCGCGAAA CAGGCGCTGA TTTGACGCTC	120
TATGACCGGT TGAACGACGA GATCATCCGG CAGATTGATA TGGCACCGCT GGGCTAACAG	180
GTGCGCAAGA TGGTGCAGCT GTATGTCTCG GACTCCGTGT CCGGATCAG CTTTGCCGAC	240
GGCCGGGTGA TCGTGTGGAG CGAGGAGCTC GCGGAGAGCC AGTATCCGAT CGAGACGCTG	300
GACGGCATCA CGCTGTTTGG GCGGCCGACG ATGACAACGC CCTTCATCGT TGAGATGCTC	360
AAGCGTGAGC GCGACATCCA GCTCTTCAG ACCGACGGCC ACTACGAGG CCGGATCTCA	420
ACACCCGACG TGTATACGC GCCGCGGCTC CGTCAGCAAG TTCACCGCAC CGAGATCTCT	480
GCGTCTGCCC TGTCGTTAAG CAACGGGATC GTGTCGAGGA AGATCCTGAA TCAGCAGGCC	540
TTGATTCCGG CACACACGTC GGGGCAAGAC GTTGCTGAGA GCATCCGCAC GATGAAGCAC	600
TCGTGCGCCT GGGTCGATCG ATCGGGCTCC CTGGCGGAGT TGAACGGGTT CGAGGGGAAAT	660
GCCGCAAAAG CATACTTAC CGCGCTGGGG CATCTCGTCC CGCAGGAGTT CGCATTTCCAG	720
GGCCGCTCGA CTCGGCCGCC GTTGGACGCC TTCAACTCGA TGGTCAGCCT CGGCTATTTCG	780
CTGCTGTACA AGAACATCAT AGGGGCGATC GAGCGTCACA GCCTGAACGC GTATATCGGT	840

205220.6481805

TTCCTACACC AGGATTACAG AGGGCACGCA ACGTCTCGTG CCGAATTCGG CACGAGCTCC	900
GCTGAAACCG CTGGCCGGCT GCTCAGTGCC CGTACGTAAT CCGCTGCCGC CAGGCCGGCC	960
CGCCGGCCGA ATACCAGCAG ATCGGACAGC GAATTGCCGC CCAGCCGGTT GGAGCCGTGC	1020
ATACCGCCGG CACACTCACC GGCAGCGAAC AGGCCTGGCA CCGTGGCGGC GCCGTGTGCC	1080
GCCTCTACTT CGACACCGCC CATCACGTAG TGACACGTCG GCCCGACTTC CATTGCCTGC	1140
GTTCGGCACG AG	1152

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CTCGTGCCGA TTCGGCAGGG TGTACTTGCC GGTGGTGTAN GCCGCATGAG TGCCGACGAC	60
CAGCAATGCG GCAACAGCAC GGATCCCGGT CAACGACGCC ACCCGGTCCA CGTGGGCGAT	120
CCGCTCAGAT CGCCCTGGG CGGCTCTTTC CTTGGGCAGG GTCATCCGAC GTGTTTCGCG	180
CGTGTTTTCG CGCCATTATG CCGGCGCGCC GCGTCGGGCG GCCGGTATGG CCGAANGTCG	240
ATCAGCACAC CCGAGATACG GGTCTGTGCA AGCTTTTGA GCGTCGCGCG GGGCAGCTTC	300
GCCGGCAATT CTACTAGCGA GAAGTCTGGC CCGATACGGA TCTGACCGAA GTCGCTGGGG	360
TGCAGCCCACT CCTATTGGC GATGGCGCCG ACGATGGCGC CTGGACCGAT CTTGTGCCGC	420
TTGCCGACGG CGACGCGGTA GGTGGTCAAG TCCGGTCTAC GCTTGGGCTT TTGCGGACGG	480
TCCCGACGCT GGTGCGGGTT GCGCCGCGAA AGCGGCGGGT CGGGTGCCAT CAGGAATGCC	540
TCACCGCCCG GGCATGCAC GGCCAGTGCC GCGGCGATGT CAGGCATCGG GACATCATGC	600
TGCGGTTTAT ACTCTCGAC CAGTCGGCGG AACAGCTCGA TTCCCGGACC GCCCA	655

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

10084843.022502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Asn Ala Val Val Ala Phe Ala Val Ile Gly Phe Ala Ser Leu Ala Val
 1 5 10 15
 Ala Val Ala Val Thr Ile Arg Pro Thr Ala Ala Ser Lys Pro Val Glu
 20 25 30
 Gly His Gln Asn Ala Gln Pro Gly Lys Phe Met Pro Leu Leu Pro Thr
 35 40 45
 Gln Gln Gln Ala Pro Val Pro Pro Pro Pro Asp Asp Pro Thr Ala
 50 55 60
 Gly Phe Gln Gly Gly Thr Ile Pro Ala Val Gln Asn Val Val Pro Arg
 65 70 75 80
 Pro Gly Thr Ser Pro Gly Val Gly Gly Thr Pro Ala Ser Pro Ala Pro
 85 90 95
 Glu Ala Pro Ala Val Pro Gly Val Val Pro Ala Pro Val Pro Ile Pro
 100 105 110
 Val Pro Ile Ile Ile Pro Pro Phe Pro Gly Trp Gln Pro Gly Met Pro
 115 120 125
 Thr Ile Pro Thr Ala Pro Pro Thr Thr Pro Val Thr Thr Ser Ala Thr
 130 135 140
 Thr Pro Pro Thr Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr
 145 150 155 160
 Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr Thr Pro Pro Thr
 165 170 175
 Thr Pro Val Thr Thr Pro Pro Thr Thr Val Ala Pro Thr Thr Val Ala
 180 185 190
 Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro
 195 200 205
 Ala Thr Ala Thr Pro Thr Thr Val Ala Pro Gln Pro Thr Gln Gln Pro
 210 215 220
 Thr Gln Gln Pro Thr Gln Gln Met Pro Thr Gln Gln Gln Thr Val Ala
 225 230 235 240
 Pro Gln Thr Val Ala Pro Ala Pro Gln Pro Pro Ser Gly Gly Arg Asn
 245 250 255
 Gly Ser Gly Gly Gly Asp Leu Phe Gly Gly Phe
 260 265

(2) INFORMATION FOR SEQ ID NO:143:

10084843.022502

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```

Ile Asn Gln Pro Leu Ala Pro Pro Ala Pro Pro Asp Pro Pro Ser Pro
1          5          10          15

Pro Arg Pro Pro Val Pro Pro Val Pro Pro Leu Pro Pro Ser Pro Pro
          20          25          30

Ser Pro Pro Thr Gly Trp Val Pro Arg Ala Leu Leu Pro Pro Trp Leu
          35          40          45

Ala Gly Thr Pro Pro Ala Pro Pro Val Pro Pro Met Ala Pro Leu Pro
          50          55          60

Pro Ala Ala Pro Leu Pro Pro Leu Pro Pro Leu Pro Pro Leu Pro Thr
          65          70          75          80

Ser His Pro Pro Arg Pro Pro Ala Pro Pro Ala Pro Pro Ala Pro Pro
          85          90          95

Ala Cys Pro Phe Val Pro Val Pro Pro Ala Pro Pro Leu Pro Pro Ser
          100          105          110

Pro Pro Thr Glu Leu Pro Ala Asp Ala Ala Cys Pro Pro Ala Pro Pro
          115          120          125

Ala Pro Pro Leu Ala Pro Pro Ser Pro Pro Ala Gly Ser Ala Ala Ile
          130          135          140

Arg Ala Leu Thr Gly Ala Thr Ser Ala Ser Thr Leu Gly His Arg Ala
          145          150          155          160

Leu Pro Asp Asp Thr Thr Ala Arg Gly Cys Arg Arg Thr Gly
          165          170

```

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

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Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly
1 5 10 15

Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg
20 25 30

Asn Arg Arg
35

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu
1 5 10 15

Cys Arg Arg Pro Ala Met Arg Gln Gln His Gly Ser Arg Ser Thr Thr
20 25 30

Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu
35 40 45

Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala
50 55 60

Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp
65 70 75 80

Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala
85 90 95

Gly Gln Leu Arg Arg Gln Phe Tyr
100

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PCR primer"
- (vi) ORIGINAL SOURCE:

10084813.022502

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGATCCTGCA GGCTCGAAAC CACGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

10084847.022502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CTCTGAATTC AGCGCTGGAA ATGTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAGAGAATTC TCAGAAGCCC ATTTGCGAGG ACA

33

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(ix) FEATURE:

1081813.02502

(A) NAME/KEY: CDS

(B) LOCATION: 152..1273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCACCGA ACAGCTGTTG TCCTCGCCGA	60
AGCATGCGGA AACCGCCCG TACGTCGCCG GACTGTGCGG GGACGTCAAG GACGCCAAGC	120
CGCGAAATTG AAGAGCACAG AAAGGTATGG C GTG AAA ATT CGT TTG CAT ACG	172
Val Lys Ile Arg Leu His Thr	
1 5	
CTG TTG GCC GTG TTG ACC GCT GCG CCG CTG CTG CTA GCA GCG GCG GGC	220
Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Ala Ala Gly	
10 15 20	
TGT GGC TCG AAA CCA CCG AGC GGT TCG CCT GAA ACG GGC GCC GGC GCC	268
Cys Gly Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala	
25 30 35	
GGT ACT GTC GCG ACT ACC CCC GCG TCG TCG CCG GTG ACG TTG GCG GAG	316
Gly Thr Val Ala Thr Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu	
40 45 50 55	
ACC GGT AGC ACG CTG CTC TAC CCG CTG TTC AAC CTG TGG GGT CCG GCC	364
Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala	
60 65 70	
TTT CAC GAG AGG TAT CCG AAC GTC ACG ATC ACC GCT CAG GGC ACC GGT	412
Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Gln Gly Thr Gly	
75 80 85	
TCT GGT GCC GGG ATC GCG CAG GCC GCC GCC GGG ACG GTC AAC ATT GGG	460
Ser Gly Ala Gly Ile Ala Gln Ala Ala Ala Gly Thr Val Asn Ile Gly	
90 95 100	
GCC TCC GAC GCC TAT CTG TCG GAA GGT GAT ATG GCC GCG CAC AAG GGG	508
Ala Ser Asp Ala Tyr Leu Ser Glu Gly Asp Met Ala Ala His Lys Gly	
105 110 115	
CTG ATG AAC ATC GCG CTA GCC ATC TCC GCT CAG CAG GTC AAC TAC AAC	556
Leu Met Asn Ile Ala Leu Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn	
120 125 130 135	
CTG CCC GGA GTG AGC GAG CAC CTC AAG CTG AAC GGA AAA GTC CTG GCG	604
Leu Pro Gly Val Ser Glu His Leu Lys Leu Asn Gly Lys Val Leu Ala	
140 145 150	
GCC ATG TAC CAG GGC ACC ATC AAA ACC TGG GAC GAC CCG CAG ATC GCT	652
Ala Met Tyr Gln Gly Thr Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala	
155 160 165	
GCG CTC AAC CCC GGC GTG AAC CTG CCC GGC ACC GCG GTA GTT CCG CTG	700
Ala Leu Asn Pro Gly Val Asn Leu Pro Gly Thr Ala Val Val Pro Leu	

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170					175					180							
CAC His	CGC Arg	TCC Ser	GAC Asp	GGG Gly	TCC Ser	GGT Gly	GAC Asp	ACC Thr	TTC Phe	TTG Leu	TTC Phe	ACC Thr	CAG Gln	TAC Tyr	CTG Leu	748	
185					190					195							
TCC Ser	AAG Lys	CAA Gln	GAT Asp	CCC Pro	GAG Glu	GGC Gly	TGG Trp	GGC Gly	AAG Lys	TCG Ser	CCC Pro	GGC Gly	TTC Phe	GGC Gly	ACC Thr	796	
200					205					210							
ACC Thr	GTC Val	GAC Asp	TTC Phe	CCG Pro	GCG Ala	GTG Val	COG Pro	GGT Gly	GCG Ala	CTG Leu	GGT Gly	GAG Glu	AAC Asn	GGC Gly	AAC Asn	844	
220					225					230							
GGC Gly	GGC Gly	ATG Met	GTG Val	ACC Thr	GGT Gly	TGC Cys	GCC Ala	GAG Glu	ACA Thr	CCG Pro	GGC Gly	TGC Cys	GTG Val	GCC Ala	TAT Tyr	892	
235					240					245							
ATC Ile	GGC Gly	ATC Ile	AGC Ser	TTC Phe	CTC Leu	GAC Asp	CAG Gln	GCC Ala	AGT Ser	CAA Gln	CGG Arg	GGA Gly	CTC Leu	GGC Gly	GAG Glu	940	
250					255					260							
GCC Ala	CAA Gln	CTA Leu	GGC Gly	AAT Asn	AGC Ser	TCT Ser	GGC Gly	AAT Asn	TTC Phe	TTG Leu	TTG Leu	CCC Pro	GAC Asp	GCG Ala	CAA Gln	988	
265					270					275							
AGC Ser	ATT Ile	CAG Gln	GCC Ala	GCG Ala	GCG Ala	GCT Ala	GGC Gly	TTC Phe	GCA Ala	TCG Ser	AAA Lys	ACC Thr	CCG Pro	GCG Ala	AAC Asn	1036	
280					285					290							
CAG Gln	GCG Ala	ATT Ile	TCG Ser	ATG Met	ATC Ile	GAC Asp	GGG Gly	CCC Pro	GCC Ala	CCG Pro	GAC Asp	GGC Gly	TAC Tyr	CCG Pro	ATC Ile	1084	
300					305					310							
ATC Ile	AAC Asn	TAC Tyr	GAG Glu	TAC Tyr	GCC Ala	ATC Ile	GTC Val	AAC Asn	AAC Asn	CGG Arg	CAA Gln	AAG Lys	GAC Asp	GCC Ala	GCC Ala	1132	
315					320					325							
ACC Thr	GCG Ala	CAG Gln	ACC Thr	TTG Leu	CAG Gln	GCA Ala	TTT Phe	CTG Leu	CAC His	TGG Trp	GCG Ala	ATC Ile	ACC Thr	GAC Asp	GGC Gly	1180	
330					335					340							
AAC Asn	AAG Lys	GCC Ala	TCG Ser	TTC Phe	CTC Leu	GAC Asp	CAG Gln	GTT Val	CAT His	TTC Phe	CAG Gln	CCG Pro	CTG Leu	CCG Pro	CCC Pro	1228	
345					350					355							
GCG Ala	GTG Val	GTG Val	AAG Lys	TTG Leu	TCT Ser	GAC Asp	GCG Ala	TTG Leu	ATC Ile	GCG Ala	ACG Thr	ATT Ile	TCC Ser	AGC Ser		1273	
360					365					370							
TAGCCTCGTT GACCACCACG CGACAGCAAC CTCGCTCGGG CCATCGGGCT GCTTTGCGGA																	1333
GCATGCTGGC CCGTGCCGGT GAAGTCGGCC GCGCTGGCCC GGCCATCCGG TGGTTCGGTG																	1393
GGATAGGTGC GGTGATCCCG CTGCTTCGCG TGCTCTTGCT GCTGGTGGTG CTGGTCATCG																	1453

AGGCGATGGG TGCGATCAGG CTCAACGGGT TGCATTCTT CACCGCCACC GAATGGAATC 1513
 CAGGCAACAC CTACGGCGAA ACCGTTGTCA CCGACGCGTC GCCCATCCGG TCGGCGCCTA 1573
 CTACGGGGCG TTGCGCTGA TCGTCGGGAC GCTGGCGACC TCGGCAATCG CCCTGATCAT 1633
 CGCGGTGCCG GTCTCTGTAG GAGCGGCGCT GGTGATCGTG GAACGGCTGC CGAAACGGTT 1693
 GGCCGAGGCT GTGGGAATAG TCCTGGAATT GCTCGCCGGA ATCCCAGCG TGGTCGTCGG 1753
 TTTGTGGGGG GCAATGACGT TCGGGCCGTT CATCGCTCAT CACATCGCTC CGGTGATCGC 1813
 TCACAACGCT CCCGATGTGC CGGTGCTGAA CTACTTGC GCACGCCGG GCAACGGGGA 1873
 GGGCATGTTG GTGTCCGGTC TGGTGTGGC GGTGATGGTC GTTCCATTAT TCGCCACCAC 1933
 CACTCATGAC CTGTTCCGG AGGTGCGGT GTTGCCCGG GAGGCGCGA TCGGGAATTC 1993

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Val	Lys	Ile	Arg	Leu	His	Thr	Leu	Leu	Ala	Val	Leu	Thr	Ala	Pro
1				5					10					15
Leu	Leu	Leu	Ala	Ala	Ala	Gly	Cys	Gly	Ser	Lys	Pro	Pro	Ser	Gly
			20					25					30	
Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	Ala
			35					40					45	
Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	Pro
			50					55					60	
Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn	Val
			65				70			75				80
Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln	Ala
				85					90					95
Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser	Glu
			100					105					110	
Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala	Ile
			115					120						
Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His	Leu

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130		135		140
Leu Asn Gly Lys Val	Leu Ala Ala Met Tyr	Gln Gly Thr Ile	Lys Thr	
145	150	155	160	
Trp Asp Asp Pro Gln	Ile Ala Ala Leu Asn	Pro Gly Val Asn	Leu Pro	
	165	170	175	
Gly Thr Ala Val Val	Pro Leu His Arg Ser	Asp Gly Ser Gly	Asp Thr	
	180	185	190	
Phe Leu Phe Thr Gln	Tyr Leu Ser Lys Gln	Asp Pro Glu Gly	Trp Gly	
	195	200	205	
Lys Ser Pro Gly Phe	Gly Thr Thr Val Asp	Phe Pro Ala Val	Pro Gly	
	210	215	220	
Ala Leu Gly Glu Asn	Gly Asn Gly Gly Met	Val Thr Gly Cys	Ala Glu	
	225	230	235	240
Thr Pro Gly Cys Val	Ala Tyr Ile Gly Ile	Ser Phe Leu Asp	Gln Ala	
	245	250	255	
Ser Gln Arg Gly Leu	Gly Glu Ala Gln	Leu Gly Asn Ser	Ser Gly Asn	
	260	265	270	
Phe Leu Leu Pro Asp	Ala Gln Ser Ile	Gln Ala Ala Ala	Gly Phe	
	275	280	285	
Ala Ser Lys Thr Pro	Ala Asn Gln Ala Ile	Ser Met Ile Asp	Gly Pro	
	290	295	300	
Ala Pro Asp Gly Tyr	Pro Ile Ile Asn Tyr	Glu Tyr Ala Ile	Val Asn	
	305	310	315	320
Asn Arg Gln Lys Asp	Ala Ala Thr Ala Gln	Thr Leu Gln Ala	Phe Leu	
	325	330	335	
His Trp Ala Ile Thr	Asp Gly Asn Lys Ala	Ser Phe Leu Asp	Gln Val	
	340	345	350	
His Phe Gln Pro Leu	Pro Pro Ala Val Val	Lys Leu Ser Asp	Ala Leu	
	355	360	365	
Ile Ala Thr Ile Ser	Ser			
	370			

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10084043.022502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCACCAGA ACAGCTGTTC TCCTCGCCGA	60
AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTGGGG GGACGTCAAG GACGCCAAGC	120
CGGAAATATG AAGAGCACAG AAAGGTATGG CGTGAAATAT CGTTTGACATA CGCTGTTGGC	180
CGTGTGTGACC GCTGCGCCGC TGCTGCTAGC AGCGGCGGGC TGTGGCTCGA AACCCAGAG	240
CGGTTGCGCT GAAACGGGCG CCGGCGCCGG TACTGTGCGG ACTACCCCGC CGTCGTCGCC	300
GGTGACGTTG GCGGAGACCG GTAGCACGCT GCTCTACCCG CTGTTCAACC TGTGGGGTCC	360
GGCCTTTTAC GAGAGGTATC CGAACGTCAC GATCACCGCT CAGGGCACCG GTTCTGGTGC	420
CGGGATCGCG CAGGCGCCGC CCGGACCGGT CAACATTGGG GCCTCCGACG CCTATCTGTC	480
GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT GATGAACATC GCGTAGGACA TCCTCCGCTCA	540
GCAGGTCAAC TACAACCTGC CCGGAGTGAG CGAGCACCTC AAGCTGAACG GAAAGTCTCT	600
GGCGGCCATG TACCAGGGCA CCATCAAAAC CTGGGACGAC CCGCAGATCG TCGCGCTCAA	660
CCCCGGCGTG AACCTGCCGC GCACCGCGGT AGTTCCGCTG CACCGTCCG ACGGGTCCGG	720
TGACACCTTC TTGTTACCCC AGTACCTGTC CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC	780
GCCCCGCTTC GGCACCAACG TCGACTTCCC GCGGTGCGCG GGTGCGCTGG GTGAGAACCG	840
CAACGGCGCG ATGGTGACCG GTTGCGCCGA GACACCGGGC TGCCTGCGCT ATATCGGCAT	900
CAGCTTCTCT GACCAGGCCA GTCAACGGGG ACTCGCGGAG GCCCAACTAG GCAATAGCTC	960
TGGCAATTTT TTGTTGCCCG ACGCGCAAAG CATTGAGGCC GCGGCGGCTG GCTTCGCATC	1020
GAAAACCCCG GCGAACGAGG CGATTTCGAT GATCGACGGG CCCGCCCCCG ACGGCTACCC	1080
GATCATCAAC TACGAGTACG CCATCGTCAA CAACCGCAA AAGGACGCCG CCACCGCGCA	1140
GACCTTGCAG GCATTTCTGC ACTGGGCGAT CACCGACGGC AACAGGCGT CGTTCCTCGA	1200
CCAGGTTTAT TTCCAGCCGC TGCCGCCCGC GGTGGTGAAG TTGCTGACG CGTTGATCGC	1260
GACGATTTCC AGCTAGCCTC GTTGACCACC ACGCGACAGC AACCTCCGTC GGGCCATCGG	1320
GCTGCTTTGC GGAGCATGCT GGCCCCGTGCC GGTGAAGTCG GCCCGCTGG CCCGCCCATC	1380
CGGTGGTTGG GTGGGATAGG TGCGGTGATC CCGCTGCTTG CGCTGGCTT GGTGCTGGTG	1440
GTGCTGGTCA TCGAGGCGAT GGGTGCGATC AGGCTCAACG GGTTCATTT CTTCACCGCC	1500
ACCGAATGGA ATCCAGGCAA CACCTACGGC GAAACCGTTG TCACCGACGC GTCGCCCATC	1560
CGGTGCGCGC CTACTACGGG GCGTTGCCGC TGATGTCGG GACGCTGGCG ACCTCGGCAA	1620

TCGCCCTGAT CATCGCGGTG CCGGTCTCTG TAGGAGCGGC GCTGGTGATC GTGGAACGGC 1680
 TGCCGAAACG GTTGGCCGAG GCTGTGGGAA TAGTCCTGGA ATTGCTCGCC GGAATCCCCA 1740
 CGGTGGTCGT CGGTTTGTGG GGGGCAATGA CGTTCGGGCC GTTCATCGCT CATCACATCG 1800
 CTCGGTGAT CGCTCACAAAC GCTCCCGATG TGCCGGTGCT GAACTACTTG CGCGGCGACC 1860
 CGGGCAACGG GGAGGGCATG TTGGTGTCCG GTCTGGTGTT GGCGGTGATG GTCGTTCCCA 1920
 TTATCGCCAC CACCACTCAT GACCTGTTC GGCAGGTGCC GGTGTTGCC CGGGAGGGCG 1980
 CGATCGGGAA TTC 1993

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1 5 10 15
 Leu Leu Leu Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
 20 25 30
 Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 35 40 45
 Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 50 55 60
 Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 65 70 75 80
 Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85 90 95
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 100 105 110
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 115 120 125
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 130 135 140
 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
 145 150 155 160

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Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 165 170 175
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Gly Gly Trp Gly
 195 200 205
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe
 275 280 285
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser
 370

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGTCTTGACC ACCACCTGGG TGTCGAAGTC GGTGCCCGGA TTGAAGTCCA GGTACTCGTG 60
 GGTGGGGCGG GCGAAACAAT AGCGACAAGC ATGCGAGCAG CCGCGGTAGC CGTTGACGGT 120

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GTAGCGAAAC GGCAACGCGG CCGCGTTGGG CACCTTGTTT AGCGCTGATT TGCACAACAC	180
CTCGTGGAAG GTGATGCCGT CGAATTGTGG CGCGCGAACG CTGCGGACCA GGCCGATCOG	240
CTGCAACCCG GCAGCGCCCG TCGTCAACGG GCATCCCGTT CACCGCGACG GCTTGCCGGG	300
CCCAACGCAT ACCATTATTC GAACAACCGT TCTATACTTT GTCAACGCTG GCCGCTACCG	360
AGCGCCGCAC AGGATGTGAT ATGCCATCTC TGCCCGCACA GACAGGAGCC AGGCCTTATG	420
ACAGCATTCC GCGTCGAGCC CTACGGGCAG CCGAAGTACC TAGAAATCGC CGGGAAGCGC	480
ATGGCGTATA TCGACGAAGG CAAGGGTGAC GCCATCGTCT TTCAGCACGG CAACCCACG	540
TCGTCTTACT TGTGGCGCAA CATCATGCCG CACTTGGAAG GGCTGGGCCG GCTGTGGCC	600
TGCGATCTGA TCGGGATGGG CGCGTCGGAC AAGCTCAGCC CATCGGACC GACCCGCTAT	660
AGCTATGGCG AGCAACGAGA CTTTTGTTC GCGCTCTGGG ATCGCTCGCA CCTCGCGCAC	720
CACGTGGTAC TGGTGCTGCA CGACTGGGGC TCGGCGCTCG GCTTCGACTG GGCTAACCAG	780
CATCGCGACC GAGTGCAGGG GATCGCGTTC ATGGAAGCGA TCGTCACCCC GATGACGTGG	840
GCGGACTGGC CGCCGCGCGT GCGGGGTGTG TTCCAGGGTT TCCGATCGCC TCAAGGCGAG	900
CCAAATGGCGT TGGAGCACAA CATCTTTGTC GAACGGGTGC TGCCCGGGGC GATCTGCGA	960
CAGCTCAGCG ACGAGGAAAT GAACCACTAT CGGCGGCCAT TCGTGAACGG CGGCGAGGAC	1020
CGTCGCCCCA CGTTGTCGTG GCCACGAAAC CTTCGAATCG ACGGTGAGCC CGCCGAGGTC	1080
GTGCGGTTGG TCAACGAGTA CCGGAGCTGG CTCGAGGAAA CCGACATGCC GAAACTGTTC	1140
ATCAACGCCG AGCCCGGGGC GATCATCACC GGCCGCATCC GTGACTATGT CAGGAGCTGG	1200
CCCAACGAGA CCGAAATCAC AGTGCCCGGC GTGCATTTCG TTCAGGAGGA CAGCGATGGC	1260
GTGCTATCGT GGGCGGGCGC TCGGCAGCAT CGGCGACCTG GGAGCGCTCT CATTCACGA	1320
GACCAAGAAT GTGATTTCOG GCGAAGGCGG CGCCCTGCTT GTCAACTCAT AAGACTTCCT	1380
GCTCCGGGCA GAGATTCTCA GGGAAAAGGG CACCAATCGC AGCGCTTCC TTCGCAACGA	1440
GGTCGACAAA TATACGTGGC AGGACAAAGG TCTTCTATT TGCCAGCGA ATTAGTCGCT	1500
GCCTTTCTAT GGGCTCAGTT CGAGGAAGCC GAGCGGATCA CGCGTATCCG ATTGGACCTA	1560
TGGAACCCGT ATCATGAAAG CTTCGAATCA TTGGAACAGC GGGGGCTCCT GCGCCGTCCG	1620
ATCATCCAC AGGGCTGCTC TCACAACGCC CACATGTACT ACGTGTFACT AGCGCCACGC	1680
GCCGATCGGG AGGAGGTGCT GCGCGCTCTG ACGAGCGAAG GTATAGGCGC GGTCTTTCAT	1740

TACGTGCCGC TTCACGATTC GCCGGCCGGG CGTCGCT

1777

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GAGATTGAAT CGTACCGGTC TCCTTAGCGG CTCGCTCCCG TGAATGCCCA TATCACGCAC	60
GGCCATGTTT TGGCTGTGCA CTTTCGCCCC ATGCCCGGAC GTTGTTAAAC CCAGGGTTTG	120
ATCASTAATT CCGGGGACG GTTGCGGGAA GCGGCCAGG ATGTGCGTGA GCCGCGGCGC	180
CGCCGTCGCC CAGGCGACCG CTGGATGCTC AGCCCCGGTG CGGCGACGTA GCCACGTTT	240
GGCGCGTGTC GTCCACAGTG GTACTCCGGT GACGACGCG CGCGGTGCCT GGGTGAAGAC	300
CGTGACCGAC GCGCGCGATT CAGA	324

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GCGGTACCGC CGCGTTGCGC TGGCACGGGA CCTGTACGAC CTGAACCACT TCGCCTCGCG	60
AACGATTGAC GAACCGCTCG TCGCGCGGCT GTGGGTGCTC AAGGTGTGGG GTGATGTCGT	120
CGATGACCGG CGCGGCACCC GGCCACTACG CGTCGAAGAC GTCCTCGCGC CCGCAGCGA	180
GCACGACTTC CAGCCCGACT CGATCGGCGT GCTGACCCGT CCTGTGCTA TGGCTGCCTG	240
GGAAGCTCGC GTTCGGAAGC GATTTGCGTT CCTCACTGAC CTCGACCGCG ACGAGCAGCG	300
GTGGGCCCGC TGCAGCAAC GGCACCGCG CGAAGTGAGG AACCGCTGG CGGTGCTGCG	360
GTCTCTATCA ACCTGCCGGC GATCGTGCCG TTCCGCTGGC ACGGTTGCGG CTGGACGCGG	420
CTGAATCGAC TAGATGAGAG CAGTTGGGCA CGAATCCGGC TGTGGTGGTG AGCAAGACAC	480
GAGTACTGTC ATCACTATTG GATGCACTGG ATGACCGGCC TGATTCAGCA GGACCAATGG	540
AACTGCCCGG GGCAAAACGT CTCGGAGATG ATCGGCGTCC CCTCGGAACC CTGCGGTGCT	600
GCGTCATTC GGACATCGGT CCGGCTCGCG GGATCGTGGT GACGCCAGCG CTGAAGGAGT	660

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GGAGCGCGCG GGTGCACGCG CTGCTGGACG GCCGCGCAGAC GGTGCTGCTG CGTAAGGGCG 720
 GGATCGCGCA GAAGCGCTTC GAGGTGGCGG CCCACGAGTT CTGTGTGTTT CCGACGGTCG 780
 CGCACAGCCA CGCCGAGCGG GTTCGCCCCG AGCACCOCGA CCTGCTGGGC CCGGCGGCCG 840
 CCGACAGCAC CGACGAGTGT GTGCTACTGC GGGCCGCGAG GAAAGTTGTT GCCGCACTGC 900
 CGGTTAACCG GCCAGAGGGT CTGGACGCCA TCGAGGATCT GCACATCTGG ACCGCCGAGT 960
 CGGTGCGCGC CGACCGGCTC GACTTTCGGC CCAAGCACAA ACTGGCCGTC TTGTGGTCT 1020
 CGGCGATCCC GCTGGCCGAG CCGGTCCGCG TGGCGCGTAG GCCCGAGTAC GCGGGTTGCA 1080
 CCAGCTGGGT GCAGCTGCCG GTGACGCCGA CGTTGGCGGC GCCGGTGCAC GACGAGGCCG 1140
 CGCTGGCCGA GGTGCGCGCC CGGGTCCGCG AGGCCGTGGG TTGACTGGGC GGCATCGCTT 1200
 GGGTCTGAGC TGTACGCCCA GTCGGCGCTG CGAGTGATCT GCTGTCGGTT CGGTCCCTGC 1260
 TGGCGTCAAT TGACGGCGCG GGCAACAGCA GCATTGGCGG CGCCATCCTC CGCGCGGCCG 1320
 GCGCCACCGC CTACAACC 1338

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CCGCGCGCAC CGGCGGCACC GCGGGTACCG GCGGCAACGG CGCTGACGCC GCTGCTGTGG 60
 TGGGCTTCGG CGCGAACGGC GACCCTGGCT TCGCTGGCGG CAAAGCGGTT AACGCGGAA 120
 TAGGTGGGGC CGCGGTGACA GCGGGGGTCG CCGCGCAGCG CGGCACCGGC GGCAAAGGTG 180
 GCACCGGCGG TGCCGGCGGC GCCGGCAACG ACGCCGGCAG CACCGGCAAT CCCGGCGGTA 240
 AGGCGGCGCA CGGCGGGATC GCGGTGCGG GCGGGGCCGG CCGCGCGGCC GGCAACGGCA 300
 ACGCGGCCCA TGCCGGCAAC C 321

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GAAGACCCGG CCCC GCCATA TGATCGGCT CGCCGACTAC TTTCGCCGAA CGTGCACGGC	60
GCGGCGTGG GCTGATCATC ACCGGTGGCT ACGCGCCCAA CCGCACCGBA TGGTGTCTGC	120
CGTTGCGCTC CGAACTCGTC ACTTCGGCGC AAGCCCGACG GCACCGCCGA ATCACCAGGG	180
CGGTCCACGA TTCCGGTGCA AAGATCCTGC TGCAAATCCT GCACGCGCGA CGCTACGCCT	240
ACCACCCACT TGCGGTCAGC GCCTCGCCGA TCAAGGCGCC GATCACCCCG TTTCGTCCGC	300
GAGCACTATC GGCTCGCGGG GTCGAAGCGA CCATCGCGGA TTTCGCCCGC TGCGCGCAGT	360
TGGCCCGCGA TGCCGGCTAC GACGCGCTCG AAATCATGGG CAGCGAAGGG TATCTGTCTA	420
ATCAGTTCCT GGGCCGCGC ACCAACAAGC GCACCGACTC GTGGGGCGGC ACACCGGCCA	480
ACCGTCGCCG GT	492

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Phe Ala Gln His Leu Val Glu Gly Asp Ala Val Glu Leu Trp Arg Ala	
1 5 10 15	
Asn Ala Ala Asp Gln Ala Asp Pro Leu Gln Pro Gly Ser Ala Arg Arg	
20 25 30	
Gln Arg Ala Ser Arg Ser Pro Arg Arg Leu Ala Gly Pro Asn Ala Tyr	
35 40 45	
His Tyr Ser Asn Asn Arg Ser Ile Leu Cys Gln Arg Trp Pro Leu Pro	
50 55 60	
Ser Ala Ala Gln Asp Val Ile Cys His Leu Cys Pro His Arg Gln Glu	
65 70 75 80	
Pro Gly Leu Met Thr Ala Phe Gly Val Glu Pro Tyr Gly Gln Pro Lys	
85 90 95	
Tyr Leu Glu Ile Ala Gly Lys Arg Met Ala Tyr Ile Asp Glu Gly Lys	
100 105 110	
Gly Asp Ala Ile Val Phe Gln His Gly Asn Pro Thr Ser Ser Tyr Leu	
115 120 125	
Trp Arg Asn Ile Met Pro His Leu Glu Gly Leu Gly Arg Leu Val Ala	

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130	135	140
Cys Asp Leu Ile Gly Met Gly Ala Ser Asp Lys Leu Ser Pro Ser Gly 145 150 155 160		
Pro Asp Arg Tyr Ser Tyr Gly Glu Gln Arg Asp Phe Leu Phe Ala Leu 165 170 175		
Trp Asp Ala Leu Asp Leu Gly Asp His Val Val Leu Val Leu His Asp 180 185 190		
Trp Gly Ser Ala Leu Gly Phe Asp Trp Ala Asn Gln His Arg Asp Arg 195 200 205		
Val Gln Gly Ile Ala Phe Met Glu Ala Ile Val Thr Pro Met Thr Trp 210 215 220		
Ala Asp Trp Pro Pro Ala Val Arg Gly Val Phe Gln Gly Phe Arg Ser 225 230 235 240		
Pro Gln Gly Glu Pro Met Ala Leu Glu His Asn Ile Phe Val Glu Arg 245 250 255		
Val Leu Pro Gly Ala Ile Leu Arg Gln Leu Ser Asp Glu Glu Met Asn 260 265 270		
His Tyr Arg Arg Pro Phe Val Asn Gly Gly Glu Asp Arg Arg Pro Thr 275 280 285		
Leu Ser Trp Pro Arg Asn Leu Pro Ile Asp Gly Glu Pro Ala Glu Val 290 295 300		
Val Ala Leu Val Asn Glu Tyr Arg Ser Trp Leu Glu Glu Thr Asp Met 305 310 315 320		
Pro Lys Leu Phe Ile Asn Ala Glu Pro Gly Ala Ile Ile Thr Gly Arg 325 330 335		
Ile Arg Asp Tyr Val Arg Ser Trp Pro Asn Gln Thr Glu Ile Thr Val 340 345 350		
Pro Gly Val His Phe Val Gln Glu Asp Ser Asp Gly Val Val Ser Trp 355 360 365		
Ala Gly Ala Arg Gln His Arg Arg Pro Gly Ser Ala Leu Ile Ser Arg 370 375 380		
Asp Gln Glu Cys Asp Phe Arg Arg Arg Arg Pro Ala Cys Gln Leu 385 390 395 400		
Ile Arg Leu Pro Ala Pro Gly Arg Asp Ser Gln Gly Lys Gly His Gln 405 410 415		
Ser Gln Pro Leu Pro Ser Gln Arg Gly Arg Gln Ile Tyr Val Ala Gly 420 425 430		

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Gln Arg Ser Ser Tyr Leu Pro Ser Glu Leu Val Ala Ala Phe Leu Trp
 435 440 445

Ala Gln Phe Glu Glu Ala Glu Arg Ile Thr Arg Ile Arg Leu Asp Leu
 450 455 460

Trp Asn Arg Tyr His Glu Ser Phe Glu Ser Leu Glu Gln Arg Gly Leu
 465 470 475 480

Leu Arg Arg Pro Ile Ile Pro Gln Gly Cys Ser His Asn Ala His Met
 485 490 495

Tyr Tyr Val Leu Leu Ala Pro Ser Ala Asp Arg Glu Glu Val Leu Ala
 500 505 510

Arg Leu Thr Ser Glu Gly Ile Gly Ala Val Phe His Tyr Val Pro Leu
 515 520 525

His Asp Ser Pro Ala Gly Arg Arg
 530 535

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Asn Glu Ser Ala Pro Arg Ser Pro Met Leu Pro Ser Ala Arg Pro Arg
 1 5 10 15

Tyr Asp Ala Ile Ala Val Leu Leu Asn Glu Met His Ala Gly His Cys
 20 25 30

Asp Phe Gly Leu Val Gly Pro Ala Pro Asp Ile Val Thr Asp Ala Ala
 35 40 45

Gly Asp Asp Arg Ala Gly Leu Gly Val Asp Glu Gln Phe Arg His Val
 50 55 60

Gly Phe Leu Glu Pro Ala Pro Val Leu Val Asp Gln Arg Asp Asp Leu
 65 70 75 80

Gly Gly Leu Thr Val Asp Trp Lys Val Ser Trp Pro Arg Gln Arg Gly
 85 90 95

Ala Thr Val Leu Ala Ala Val His Glu Trp Pro Pro Ile Val Val His
 100 105 110

Phe Leu Val Ala Glu Leu Ser Gln Asp Arg Pro Gly Gln His Pro Phe
 115 120 125

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Asp Lys Asp Val Val Leu Gln Arg His Trp Leu Ala Leu Arg Arg Ser
130 135 140

Glu Thr Leu Glu His Thr Pro His Gly Arg Arg Pro Val Arg Pro Arg
145 150 155 160

His Arg Gly Asp Asp Arg Phe His Glu Arg Asp Pro Leu His Ser Val
165 170 175

Ala Met Leu Val Ser Pro Val Glu Ala Glu Arg Arg Ala Pro Val Val
180 185 190

Gln His Gln Tyr His Val Val Ala Glu Val Glu Arg Ile Pro Glu Arg
195 200 205

Glu Gln Lys Val Ser Leu Leu Ala Ile Ala Ile Ala Val Gly Ser Arg
210 215 220

Trp Ala Glu Leu Val Arg Arg Ala His Pro Asp Gln Ile Ala Gly His
225 230 235 240

Gln Pro Ala Gln Pro Phe Gln Val Arg His Asp Val Ala Pro Gln Val
245 250 255

Arg Arg Arg Gly Val Ala Val Leu Lys Asp Asp Gly Val Thr Leu Ala
260 265 270

Phe Val Asp Ile Arg His Ala Leu Pro Gly Asp Phe
275 280

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

ATGAACATGT CGTCGGTGGT GGGTCGCAAG GCCTTTGCGC GATTCCGCCG CTACTCCTCC	60
GCCATGCACG CGATCGCCGG TTTCTCCGAT GCCTTGCCGC AAGAGCTGCG GGGTAGCGGA	120
ATCGCCGTCT CGTGATCCA CCCGGCGCTG ACCCAGACAC CGCTGTTGGC CAACGTCGAC	180
CCCGCCGACA TGCCGCCGCC GTTTCGCAGC CTCACGCCCA TTCCCGTTCA CTGGGTCGCG	240
GCAGCGGTGC TTACGGTGT GGCG	264

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TAGTCGGCGA	CGATGACGTC	GCGGTCCAGG	CCGACCGCTT	CAAGCACCAG	CGCGACCACG	60
AAGCCGGTGC	GATCCTTACC	CGCGAAGCAG	TGGGTGAGCA	CCGGGCGTCC	GGCGGCAAGC	120
AGTGTGACGA	CACGATGTAG	CGCGCGCTGT	GCTCCATTGC	CGGTTGGGAA	TTGGCGATAC	180
TCGTCGGTCA	TGTAGCGGGT	GGCCGCGTCA	TTTATCGACT	GGCTGGATTG	GCCGGACTCG	240
CCGTTGGACC	CGTCATTGGT	TAGCAGCCTC	TTGAATCGGG	TTTCGTGCGG	CGCTGAGTCG	300
TCGGCGTCAT	CATCGGCAGG	GTGCGGGAAC	GGCAGCAGGT	GGACGTCGAT	GCCGTCGGGA	360
ACCCGCTCTG	GACCGCGCGG	GGCAACCTCC	CGGGACGACC	GCAGGTCGGC	AACGTCGGTG	420
ATCCCCAGCC	GGCGCAGCGT	TGCCCCCTCG	GCCGAATTCG	GCACGAGGCT	GGCGAGCCAC	480
CGGGCATCAC	CAAGCAACGC	TTGCCAGTA	CGGATCGTCA	CTTCCGCATC	CGGCAGACCA	540
ATCTCTCGC	CGCCCATCGT	CAGATCCGCG	TCGTGCGTTG	ACAAGAACGG	CCGCAGATGT	600
GCCAGCGGGT	ATCGGAGATT	GAACCGCGCA	CGCAGTTCTT	CAATGCTGCG	GCGCTGCCGC	660
ACTATTGGCA	CTTTCCGGCG	GTGCGGTTAT	TCAGCAAGCA	TGCGAGTCTC	GACGAACTCG	720
CCCCACGTAA	CCCACGGCGT	AGCTCCCGGC	GTGACGCGGA	GGATCGGCGG	GTGATCTTTG	780
CGGCCACGCT	CGTAGCCGTT	GATCCACC GC	TTGCGGTTGC	CGGCGGGGAG	GCCGATCAGC	840
TTATCGACCT	CGGCGTATGC	CGACGGCAAG	CTGGGCGCGT	TCGTCGAGGT	CAAGAACTCC	900
ACCATCGGCA	CCGGCACCAA	GGTGCCGCAC	CTGACCTACG	TCGCGCAGCG	GCACATCGGC	960
GAGTACAGCA	ACATCGGCGC	CTCAGCGGTG	TTGTCCTAAT	ACGACGGTAC	GTCCAAACGG	1020
CGCACCAACG	TCGGTTCGCA	CGTACGGACC	GGGTCCGACA	CCATGTTCTG	GGCCCCAGTA	1080
ACCATCGGCG	ACGGCGCGTA	TACCGGGGCC	GGCAGAGTGG	TGCGGGAGGA	TGTCGCCGCG	1140
GGGGCGCTGG	CAGTGTCCGG	GGGTCCGCAA	C			1171

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

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GCAAAGGCGG CACCGGCGGG GCGGCATGA ACAGCCTCGA CCCGCTGCTA GCGCCCCAAG 60
 ACGGCGGCCA AGGCGGCACC GCGGCACCG GCGGCAACGC CGGCGCCGGC GGCACCAGCT 120
 TCACCCAAGG CGCCGACGGC AACGCCGGCA ACGGCGGTGA CGGCGGGGTC GCGGCAACG 180
 GCGGAAACGG CGGAAACGGC GCAGACAACA CCACCACCGC CGCGCGC 227

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CCTCGCCACC ATGGGCGGSC AGGGCGGTAG CGGTGGCGCC GGCTCTACCC CAGGCGCCAA 60
 GGGCGCCAC GGCCTTCACT CAACCAGCGG CGGCGACGGC GGCAGCGCGC GCAACGGCGG 120
 CAACTCCCAA GTGGTCGGCG GCAACGGCGG CGACGGCGGC AATGGCGGCA ACGGCGGCAG 180
 CGCGGCACG GCGGCAACG GCGGCCGCGG CGGCGACGGC GCGTTTGGTG GCATGAGTGC 240
 CAACGCCACC AACCCTGGTG AAAACGGGCC AAACGGTAAC CCCGGCGGCA ACGGTGGCGC 300
 CGGC 304

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GTGGGACGCT GCCGAGGCTG TATAACAAGG ACAACATCGA CCAGCGCCGG CTCGGTGAGC 60
 TGATCGACCT ATTTAACAGT GCGCGCTTCA GCGGCGAGGG CGAGCACCGC GCCCGGGATC 120
 TGATGGGTGA GGTCTACGAA TACTTCCTCG GCAATTTCGC TCGCGCGGAA GGAAGCGGG 180
 GTGGCGAGTT CTTTACCCCG CCCAGCGTGG TCAAGGTGAT CGTGGAGGTG CTGGAGCCGT 240
 CGAGTGGGCG GGTGTATGAC CCGTGCTGCG GTTCCGGAGG CATGTTTGTC CAGACCGAGA 300
 AGTTCATCTA CGAACACGAG GCGGATCCGA AGGATGTCTC GATCTATGGC CAGGAAAGCA 360
 TTGAGGAGAC CTGGCGGATG GCGAAGATGA ACCTGCGCAT CCACGGCATC GACAACAAGG 420

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GGCTCGGCGC CCGATGGAGT GATACCTTCG CCCGCGACCA GCACCCGGAC GTGCAGATGG 480
 ACTACGTGAT GGCCAATCCG CCGTTCAACA TCAAAGACTG GGCCCGCAAC GAGGAAGACC 540
 CACGCTGGCG CTTCCGGTGT CCGCCCCGCA ATAACGCCAA CTACGCATGG ATTCAGCACA 600
 TCCTGTACAA CTTGGCGCCG GGAGGTCGGG CGGGCGTGCT GATGGCCAAC GGGTCGATGT 660
 CGTCGAATC CAACGGCAAG GGGGATATTC GCGCGCAAA CTGTGGAGGCG GATTGTGTTT 720
 CTTGCATGGT CCGCTTACCC ACCCAGCTGT TCCGCAGCAC CGGAATCCCG GTGTGCCTGT 780
 GGTTTTTCGC CAAAAACAAG GCGGCAGGTA AGCAAGGGTC TATCAACCGG TCGGGGCAGG 840
 TGCTGTCAT CGACGCTCGT GAACTGGGCG ACCTAGTGGA CCGGGCCGAG CGGGCGCTGA 900
 CCAACGAGGA GATCGTCCG ATCGGGGATA CCTTCCACGC GAGCACGACC ACCGGCAACG 960
 CCGGCTCCCG TGGTGCCGGC GGTAAATGGG GCACTGGCCT CAACGGCGCG GCGGTGCTG 1020
 GCGGGGCGCG CGGCAACGCG GGTGTCGCCG GCGTGTCTT CGGCAACGCT GTGGGCGGCG 1080
 ACGGCGGCAA CGCGGGCAAC GCGGCCACG GCGGCGACGG CACGACGGCG GCGCGCGGCG 1140
 GCAAGGGCGG CAACGGCAGC AGCGGTGCCG CCAGCGGCTC AGGCGTCTGC AACGTACCCG 1200
 CCGGCCACGG CGGCAACGCG GGCAATGGCG GCAACGGCG CAACGGCTCC GCGGGCGCGG 1260
 GCGGCGAGGG CGGTGCCGGC GGCAGCGCG GCAACGGCG CCACGGCGCG GGTGCCACCG 1320
 GCGGCGCCAG CGGCAAGGGC GGCAACGGCA CCAGCGGTGC CGCCAGCGCG TCAGGCGTCA 1380
 TCAACGTAC CGCCGGCCAC GCGGCAACG GCGGCAATGG CCGCAACGGC GGCAACGGC 1439

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GGGCGGCGCG GCGCGGATTT TCTCGTGCT TGATGTGCG TGGGGATAAC GCGGTGATG 60
 GTGGTAACGG CCGGATGGCG GGGGCTGGCG GGGCTGGCG CCCCGCGGG GCGGCGGGCC 120
 TGATCAGCCT GCTGGGCGCG CAAGGCGCCG GCGGGGCGCG CGGACCGCG GGGGCGGGCG 180
 GTGTTGGCGG TGACGGCGGG GCGGCGGGCC CCGGCAACCA GGCCTTCAAC CGAGGTGCCG 240
 GCGGGGCGCG CGGCCTGATC AGCCTGCTGG GCGGCCAAGG GCGGCGCGG GCGGCGGGGA 300
 CCGGCGGGCG CGGCGGTGTT GCGGCTGAC 329

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(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GCAACGGTGG CAACGGCGGC ACCAGCACGA CCGTGGGGAT GGCCGGAGGT AACTGTGGTG 60
 CCGCCGGGCT GATCGGCAAC 80

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GGGCTGTGTC GCACCTACAC CGCCGCATTG GGCAGCTTG GCCGCCAAT ATCCAGCTCA 60
 AGGCCTACTA CTTACCGTCG GAGGACCGCC GCATCAAGGT GCGGGTCAGC GCCCAAGSAA 120
 TCAAGGTCAT CGACCGCGAC GGGCATCGAG CCGTCGTCG CGCGGCTCGG GCAGGATCCG 180
 CCCCAGCGCA CTTCGCGCGC CAAGCGGGCT CATCGCTCCG AACGGCGCGG ATCCTGTGAG 240
 CACAACCTGAT GCGCGGCAAC GAGATTCGTC CAATTGTCAA GCCGTGTTTC ACCGCAGGGA 300
 CCGGTTATAC GTATGTCAAC CTATGTCACT CGCAAGAACC GGCATAACGA TCCCCTGATC 360
 CGCCGACAGC CCACGAGTGC AAGACCGTTA CA 392

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 535 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

ACCGGCGCCA CCGCGGCGAC CGGGTTCGCC GTGGGCGCCG GCGGGGCCGG CCGGCAGGGC 60
 GGTATCAGCG GTGCCGCGCG CACCAACGCG TCTGTTGCGC CTGGCGGCAG CCGCGGACAA 120
 GCGCGCGCCG GGGGCGCTGG CGGGGCGCGC GCCGATAACC CCACCGGCAT CGGCGGCGCC 180

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GGCGGCACCG GCGGCACCG CGGAGCGGCC GGAGCCGGCG GGGCCGGTGG CGCCATCGGT 240
 ACCGGCGGCA CCGGCGGCGC GGTGGGCAGC GTCGGTAACG CCGGGATCGG CGGTACCGGC 300
 GGTACGGGTG GTGTCGGTGG TGCTGGTGGT GCAGGTGCGG CTGCGGCCGC TGGCAGCAGC 360
 GCTACCGGTG GCGCCGGGTT CGCCGGCGGC GCCGGCGGAG AAGGCGGACC GGGCGGCAAC 420
 AGCGGTGTGG GCGGCACCAA CGGCTCCGGC GCGCGCGGCG GTGCAGGCGG CAAGGCGCGC 480
 ACCGGAGGTG CCGGCGGGTC CGGCGCGGAC AACCCACCG GTGCTGGTTT CGCCG 535

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CCGACGTCGC CGGGCGGATA CGGGGGTCAC CGACTACTAC ATCATCCGCA CCGAGAATCG 60
 GCCGCTGCTG CAACCGCTGC GGGCGGTGCC GGTATCGGA GATCCGCTGG CCGACCTGAT 120
 CCAGCCGAAC CTGAAGGTGA TGCTCAACCT GGGCTACGGC GACCCGAAT ACGGCTACTC 180
 GACGAGCTAC GCCGATGTGC GAACGCCGTT CGGGCTGTGG CCGAACGTGC CGCCTCAGGT 240
 CATCGCCGAT GCCCTGGCCG CCGGAACACA AGAAGGCATC CTTGACTTCA CGGCCGACCT 300
 GCAGGCGCTG TCCGCGCAAC CGCTCACGCT CCCGCAGATC CAGCTGCCGC AACCCGCCGA 360
 TCTGTTGGCC GCGGTGGCCG CCGCACCGAC GCCGGCCGAG GTGGTGAACA CGCTCGCCAG 420
 GATCATCTCA ACCAACTACG CCGTCTGCT GCCACCGTG GACATCGCCC TCGCTCGGTC 480
 ACCACCTGCG CGTGTACAC CACCCAATG TTCGTCAGGC AACTCGCTGC GGGCAATCTG 540
 ATCAAGCGCA TCGGTATCC CCTGGCGGCC ACCGTAGGTT TAGGCACGAT CGATAGCGGG 600
 CGGCGTGGA TTGCTACCC TCCTCGCGGC GGCCTCGGAC ACCGTTGCAA ACATCGAGGG 660
 CCTCGTCACC TAACGGATTC CCGACGGCAT 690

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

205220.484800T
 10084843.022502

ACGGTGACGG CGGTACTGGC GGCGGCCACG GCGGCAACGG CGGGAATCCC GGGTGGCTCT	60
TGGGCACAGC CGGGGGTGGC GGCAACGGTG GCGCCGGCAG CACCGGTACT GCAGGTGGCG	120
GCTCTGGGGG CACCGCGGC GACGCGGGGA CCGCGGGCG TGCGGGCCTG TTAATGGCG	180
CCGGCGCCGG CGGGCACGGT GGCACTGGCG GCGCGGGCG TGCCGGTGTC GACGGTGGCG	240
GCGCCGGCGG GCGCGCGGG GCGCGGGCA ACGGCGGGCG CGGGGGTCAA GCGGCCCTGC	300
TGTCGGGGG CGCGGCCACC GCGGAGCCG GCGGCTACGG CGGCGATGGC GGTGGCGGG	360
GTGACGGCTT CGACGGCAGC ATGGCGGGCC TGGGTGGTAC CGGTGGC	407

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GATCGGTACG CGCATCGCCC TCGGCGGCAA GCGATTCCGC GGTCTCACCG AAGAACATCG	60
TGCACGCGGC GCGCGGGACC AGCCCGCTGC GCTGCGGCGC GTCGAACGCC TCCAGCAGGC	120
ACAGCCAGTC CTTGGCGGCC TCGAGGCGA ACACGTGGT GTCACCGGTG TAGATCGCG	180
GGATGCCCCG CTCGCGCAAC GCATTCCGGC ACGCCCGCGC GTCTTTGTGA TGCTCGACGA	240
TCACCGCGAT GTCTGCGGCC ACCACGGGCC GCCCGGCGAA GGTGGCCCCG CTGGCCAGTA	300
GCGCCGCGAC GTGCGGGGCC AGTCTGTCGG GGATGTGCGC GCGCAGCGCT CCGGCGCGAC	360
GCCCGAAAAA CGACCCCTCA CCCAGCTGGG TCCGCTGCGC ATATCCCTTG CCGTCTCTGG	420
CGATATTGGA CGCGCATGCC CCGACCGCGT ACAGGCCGCG CACCACCG	468

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGTGGTAACG GCGGCCAGGG TGGCATCGGC GCGCCGGCG AGAGAGGCGC CGACGCGGCC	60
GGCCCCAATG CTAACGGCGC AAACGGCGAG AACGGCGGTA GCGGTGGTAA CGGTGGCGAC	120

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GGCGGCGCCG GCGGCAATGG CGGCGCGGGC GGCAACGCGC AGGCGGCCGG GTACACCGAC 180
GGCGCCACGS GCACCGGCGG CGACGCGGCG AACGCGCGC 219

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TAGCTCCGGC GAGGCGGCA AGGCGGCGA CGGTGGCCAC GCGGTGACG GCGTCGSCGG 60
CAACAGTTCC GTCACCAAG GCGGCAGCGG CGGTGGCGGC GCGCCGCGG GCGCCGGCGG 120
CAGCGGCTTT TTCGGCGGCA AGGCGGGCTT CGCGCGCGAC GCGGTCTAGG GCGGCCCCAA 180
CGGCGGCGGT ACCGTCGGCA CCGTGGCCGG TGSCGCGCGC AACGCGCGTG TCGGCGSCCG 240
GGGCGGCGAC GGCCTCTTTG CCGGTGCCGG CGGCCAGGGC GGCCTCGGTG GGCAGGGCGG 300
CAATGGCGGC GGCCTCCACG GCGGCAACGG CGGCCTTGGC GGC CGGGCGG GTGGCGGAGG 360
CAACGCCCG GCTCGTGCCG AATCCGGGCT GACCATGGAC AGCGCGGCCA AGTTCGCTGC 420
CATCGCATCA GGC CGGTACT GCCCGAACA CCTGGAACAT CACCCGAGTT AGCGGGGCGC 480
ATTCCTGAT CACC 494

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GGCGCGGTGG TGCCGCGGGC CAGCTCTTCA GCGCCGGAGG CGCGCGGGT GCCGTGGGG 60
TTGGCGGCAC CGCGGCGCAG GSTGGGCTG GCGGTGCCGG AGCGCGCGGC GCCGACGCCC 120
CCGCCAGCAC AGGTCTAACC GGTGGTACCG GGTTCGTGG CGGGGCCGGC GCGTCGCGG 180
GCCAGAGCGG CAACGCCATT GCCGGCGGCA TCACGGGCTC 220

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 388 base pairs
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ATGGCGGCAA CGGGGGCCCC GCGGTGCTG GCGGGGCGCG CGACTACAAT TTCCAACGGC	60
GGGCAGGGTG GTGCCGGCGG CCAAGGCGGC CAAGGCGGCC TGGGCGGGGC AAGCACCACC	120
TGATCGGCCT AGCCGCACCC GGGAAAGCCG ATCCAACAGG CGACGATGCC GCCTTCCTTG	180
CCGCGTTGGA CCAGGCCGGC ATCACCCTACG CTGACCCAGG CCACGCCATA ACGGCCGCCA	240
AGGCGATGTG TGGGCTGTGT GCTAACGGCG TAACAGTCT ACAGCTGGTC GCGGACCTGC	300
GGGACTACAA TCCGGGCTG ACCATGGACA GCGCGGCCAA GTTCGCTGCC ATCGCATCAG	360
GCGGCTACTG CCCCGAACAC CTGGAACA	388

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GCAAAGGCGG CACCGGCGGG GCCGGCATGA ACAGCCTCGA CCCGCTGCTA GCCGCCCAAG	60
ACGGCGGCCA AGCGGCGACC GCGGCGACCG GCGGCAACGC CGGCGCCGGC GGCACCAGCT	120
TCACCCAAGG CGCCGACGGC AACGCCGGCA ACGGCGGTGA CGGCGGGGTC GGCGGCAACG	180
GCGGAAACGG CGGAAACGGC GCAGACAACA CCACCACCGC CGCCGCCGGC ACCACAGGGC	240
GCGAGCGCGG GCGCGGCGGG GCCGGCGGAA CCGCGGGAAC CGGCGGAGCC GCCGGCACCG	300
GCACCGGCGG CCAACAAGGC AACGGCGGCA ACGGCGGCAC CGGCGGCAAA GCGGCGCACG	360
GCGGCGACGG TGCACTCTCA GGCAGCACCG GTGGTGCCGG	400

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GGCAACGGCG GCAACGGCGG CATCGCCGCG ATTGGGCGGC AACGGCGTTC CGGGACGGGC	60
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AGCGGCAACG GCGGCCAACG GCGGCAGCGG CGGCAACGGC GGCAACGCCG GCATGGCGGG 120
 CAACAGCGCG ACCGGCAGCG GCGACGGCGG TGCCGGCGGG AACGGCGGCG CGGCGGGCAC 180
 GGGCGGCACC GGGCGGCAGC GCGGCCTCAC CGGTACTGGC GGCACCGGGC GCAGCGGTGG 240
 CACCGGCGGT GACGGCGGTA ACGGCGGCAA CGGAGCAGAT AACACCGCAA ACATGACTGC 300
 GCAGGCGGGC GGTGACGGTG GCAACGGCGG CGACGGTGGC TTCGGCGGCG GGGCGGGGGC 360
 CGGCGGCGGT GGCTTGACCG CTGGCGCCAA CGGCACCGGC GGGCAAGGCG GCGCGGGCGG 420
 CGATGGCGGC AACGGGGCCA TCGGCGGCCA CGGCCCACTC ACTGACGACC CCGCGGGCAA 480
 CGGGGGCACC GGGCGCAACG GCGGCACCGG CGGCACCGGC GGCAGGGGCA TCGGCAGC 538

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GGGCGGTGG TGCCGGGGC CAGCTCTTCA GCGCCGAGG CGCGGCGGT GCCGTGTTGG 60
 TTGGCGGCAC CGGCGGCCAG GGTGGGGCTG GCGGTGCCG AGCGGCGCG GCCGACGCCC 120
 CCGCAGCAC AGGTCTAACC GGTGGTACCG GGTTCGTGG CGGGGCGCG GCGTTCGGCG 180
 GCCACGGCG CAACGCCATT GCGGCGGCA TCAACGGCTC CGTGGTGCC GCGGCGACC 239

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

AGCAGCGCTA CCGGTGGCG CGGGTTCGCC GCGGCGCCG GCGGAGAAG CGGAGCGGGC 60
 GGCAACAGCG GTGTGGGCGG CACCAACGGC TCCGCGGCG CGGCGGTGC AGGCGGCAAG 120
 GCGGCAACG GAGGTGCCGG CGGGTCCGGC GCGGACAACC CCACCGGTG TGGTTTCGCC 180
 GGTGGCGCCG GCGGCACAGG TGGCGCGGCC GCGCCGCGG GGGCCGGCG GCGGACCGGT 240
 ACCGGCGGCA CCGGCGCGGT TGTGGCGGCC ACCGGTAGTG CAGGCATCG CGGGGCGGGC 300
 GGCCGCGGCG GTGACGGCGG CGATGGGGCC AGCGGTCTCG GCCTGGGCTT CTCCGCTTT 360

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GACGGCGGCC AAGCGGCCA AGGCGGGGCC GCGGCGAGCG CCGGCGCCGG CGGCATCAAC 420
 GGGGCGGGCG GGGCGGGCGG CAACGCGGCG GACGCGGGGG ACGGCGCAAC CGGTGCGCGA 480
 GGTCTCGGCG ACAACGGCGG GGTGCGCGGT GACGGTGGGG CCGGTGGCGC CGCGGGCAAC 540
 GGGCGCAACG CGGGCGTCGG CCTGACAGCC AAGGCGGGCG ACGGCGGGCG CGCGGGCAAT 600
 GGGCGCAACG GGGGCGCCGG CGGTGCTGGC GGGGCGGGCG ACAACAATTT CAACGGCGGC 660
 CAGGGTGGTG CCGGCGGCCA AGGCGGCCAA GCGGCGTTGG GCGGGGCAAG CACCACCTGA 720
 TCGGCCTAGC CGCAGCCGGG AAAGCCGATC CAACAGGCGA CGATGCCGCC TTCCTTGGCG 780
 CGTTGGACCA GGCGGGCATC ACCTACGCTG ACCCAGGCCA CGCCATAACG GCCGCGCAAG 840
 CGATGTGTGG GCTGTGTGCT AACGGCGTAA CAGGTCTACA GCTGTCGCG GACCTGCGGG 900
 AATAAATCC CGGGCTGACC ATGACAGCG CGGCCAAGTT CGTGCCATC GCATCAGGCG 960
 CGTACTGCCC CGAACACCTG GAACA 985

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCCCGGG TTTCCCCACC 60
 CGAGGAAAGC CGCTACCAGA TGGCGTGCC GAAGTAGGGC GATCCGTTGC CGATGCCGGC 120
 ATGAACGGGC GGCATCAAA TAGTGACGGA ACCTTTCACT TTAGCGAGCA TAATGGCTAT 180
 AGCACTAAGG AGGATGATCC GATATGACGC AGTCGACAGC CGTGACGGTG GATCAGCAAG 240
 AGATTTTGAA CAGGGCCAAC GAGGTGGAGS CCCCGATGCG GGACCCACCG ACTGATGTCC 300
 CCATCACACC GTGCGAACTC ACGGCGGCTA AAAACGCCG CCAACAGCTG GTATTGTCCG 360
 CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAGA GCGGCAGCGT CTGGCGACCT 420
 CGCTGCGCAA CGCGGCCAAG GCGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG 480
 ACAACGACGG CGAAGGAACT GTGCAGGCAG AATCGGCCGG GCGCGTCGGA GGGGACAGTT 540
 CGGCCGAAC TACCGATACG CCGAGGGTGG CCACGGCCGG TGAACCCAAC TTCATGGATC 600
 TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTTTG 660

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CGGATGGGTG GAACACTTTC AACCTGACGC TGCAAGGCGA CGTCAAGCGG TTCCGGGGGT	720
TTGACAACTG GGAAGGCGAT GCGGCTACCG CTTGCGAGGC TTCGCTCGAT CAACAACGGC	780
AATGGATACT CCACATGGCC AAATTGAGCG CTGCGATGGC CAAGCAGGCT CAATATGTCTG	840
CGCAGCTGCA CGTGTGGGCT AGCGGGGAAC ATCCGACTTA TGAAGACATA GTCGGGCTCG	900
AACGGCTTTA CGCGAAAAAC CCTTCGGCCC GCGACCAAT TCTCCCGGTG TACGCGGAGT	960
ATCAGCAGAG GTCGGAGAAG GTGCTGACCG AATACAACAA CAAGGCAGCC CTGGAACCGG	1020
TAAACCCGCC GAAGCCTCCC CCCGCCATCA AGATCGACCC GCCCCCGCCT CCGCAAGAGC	1080
AGGGATTGAT CCCTGGCTTC CTGATGCCGC CGTCTGACGG CTCCGGTGTG ACTCCCGGTA	1140
CCGGGATGCC AGCCGCACCG ATGTTTCCGC CTACCGGATC GCCCGGTGGT GGCCTCCCGG	1200
CTGACACGGC GGCAGCAGTG ACGTCGGCTG GCGGGGAAGC CGCAGCGCTG TCGGCGCAGC	1260
TGGCGGTCAA AGCGGCATCG CTCGGTGGCG GTGGAGGCGG CGGGGTGCCG TCGGCGCCGT	1320
TGGGATCCGC GATCGGGGGC GCCGAATCGG TCGGCCCCGC TGCGCTGGT GACATTGCCG	1380
GCTTAGGCCA GGAAGGGGCC GCGGCGGCGC CCGCGCTGGG CGGCGGTGGC ATGGGAATGC	1440
CGATGGGTGC CGCGCATCAG GGACAAGGGG GCGCCAAGTC CAAGGGTTCT CAGCAGGAAG	1500
ACGAGGCGCT CTACACCGAG GATCGGCGAT GGACCGAGGC CGTCATTGGT AACCTCGGC	1560
GCCAGGACAG TAAGAGTCG AAGTGAGCAT GGACGAATTG GACCCGCATG TCGCCCGGGC	1620
GTTGACGCTG GCGGCGCGGT TTCAGTCGGC CCTAGACGGG ACGCTCAATC AGATGAACAA	1680
CGGATCCTTC CGCGCCACCG ACGAAGCCGA GACCGTCGAA GTGACGATCA ATGGGCACCA	1740
GTGGCTCACC GGCCTGCACA TCGAAGATGG TTTGCTGAAG AAGCTGGGTG CCGAGGCGGT	1800
GGCTCAGCGG GTCAACGAGG CGCTGCACAA TCGCAGGCC GCGGCGTCCG CGTATAACGA	1860
CCGGCGGGC GAGCAGCTGA CCGCTGCGTT ATCGGCCATG TCCCGCGCGA TGAACGAAGG	1920
AATGGCTTAA GCCATTGTT GCGGTGTTAG CGACTACGCA CCGAATGAGC GCCGCAATGC	1980
GGTCATTGAG CGGCGCCGAC ACGGCGTGAG TACGCATTGT CAATGTTTGT ACATGGATCG	2040
GCCGGGTTTG GAGGCGGCCA TAGTCCTGGT CGCCAATATT GCGCAGCTA GCTGGTCTTA	2100
GGTTCGGTTA CGCTGGTTAA TTATGACGTC CGTTACCA	2138

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: amino acid

20520.5484001

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met	Thr	Gln	Ser	Gln	Thr	Val	Thr	Val	Asp	Gln	Gln	Glu	Ile	Leu	Asn	1	5	10	15
Arg	Ala	Asn	Glu	Val	Glu	Ala	Pro	Met	Ala	Asp	Pro	Pro	Thr	Asp	Val	20	25	30	
Pro	Ile	Thr	Pro	Cys	Glu	Leu	Thr	Ala	Ala	Lys	Asn	Ala	Ala	Gln	Gln	35	40	45	
Leu	Val	Leu	Ser	Ala	Asp	Asn	Met	Arg	Glu	Tyr	Leu	Ala	Ala	Gly	Ala	50	55	60	
Lys	Glu	Arg	Gln	Arg	Leu	Ala	Thr	Ser	Leu	Arg	Asn	Ala	Ala	Lys	Ala	65	70	75	80
Tyr	Gly	Glu	Val	Asp	Glu	Glu	Ala	Ala	Thr	Ala	Leu	Asp	Asn	Asp	Gly	85	90	95	
Glu	Gly	Thr	Val	Gln	Ala	Glu	Ser	Ala	Gly	Ala	Val	Gly	Gly	Asp	Ser	100	105	110	
Ser	Ala	Glu	Leu	Thr	Asp	Thr	Pro	Arg	Val	Ala	Thr	Ala	Gly	Glu	Pro	115	120	125	
Asn	Phe	Met	Asp	Leu	Lys	Glu	Ala	Ala	Arg	Lys	Leu	Glu	Thr	Gly	Asp	130	135	140	
Gln	Gly	Ala	Ser	Leu	Ala	His	Phe	Ala	Asp	Gly	Trp	Asn	Thr	Phe	Asn	145	150	155	160
Leu	Thr	Leu	Gln	Gly	Asp	Val	Lys	Arg	Phe	Arg	Gly	Phe	Asp	Asn	Trp	165	170	175	
Glu	Gly	Asp	Ala	Ala	Thr	Ala	Cys	Glu	Ala	Ser	Leu	Asp	Gln	Gln	Arg	180	185	190	
Gln	Trp	Ile	Leu	His	Met	Ala	Lys	Leu	Ser	Ala	Ala	Met	Ala	Lys	Gln	195	200	205	
Ala	Gln	Tyr	Val	Ala	Gln	Leu	His	Val	Trp	Ala	Arg	Arg	Glu	His	Pro	210	215	220	
Thr	Tyr	Glu	Asp	Ile	Val	Gly	Leu	Glu	Arg	Leu	Tyr	Ala	Glu	Asn	Pro	225	230	235	240
Ser	Ala	Arg	Asp	Gln	Ile	Leu	Pro	Val	Tyr	Ala	Glu	Tyr	Gln	Gln	Arg	245	250	255	
Ser	Glu	Lys	Val	Leu	Thr	Glu	Tyr	Asn	Asn	Lys	Ala	Ala	Leu	Glu	Pro	260	265	270	

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Val Asn Pro Pro Lys Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro
 275 280 285
 Pro Pro Gln Glu Gln Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser
 290 295 300
 Asp Gly Ser Gly Val Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met
 305 310 315 320
 Val Pro Pro Thr Gly Ser Pro Gly Gly Gly Leu Pro Ala Asp Thr Ala
 325 330 335
 Ala Gln Leu Thr Ser Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp
 340 345 350
 Val Ala Val Lys Ala Ala Ser Leu Gly Gly Gly Gly Gly Val
 355 360 365
 Pro Ser Ala Pro Leu Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg
 370 375 380
 Pro Ala Gly Ala Gly Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly
 385 390 395 400
 Gly Gly Ala Ala Leu Gly Gly Gly Gly Met Gly Met Pro Met Gly Ala
 405 410 415
 Ala His Gln Gly Gln Gly Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu
 420 425 430
 Asp Glu Ala Leu Tyr Thr Glu Asp Arg Ala Trp Thr Glu Ala Val Ile
 435 440 445
 Gly Asn Arg Arg Arg Gln Asp Ser Lys Glu Ser Lys
 450 455 460

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 277 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Ala Gly Asn Val Thr Ser Ala Ser Gly Pro His Arg Phe Gly Ala Pro
 1 5 10 15
 Asp Arg Gly Ser Gln Arg Arg Arg Arg His Pro Ala Ala Ser Thr Ala
 20 25 30
 Thr Glu Arg Cys Arg Phe Asp Arg His Val Ala Arg Gln Arg Cys Gly
 35 40 45

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Phe Pro Pro Ser Arg Arg Gln Leu Arg Arg Arg Val Ser Arg Glu Ala
 50 55 60
 Thr Thr Arg Arg Ser Gly Arg Arg Asn His Arg Cys Gly Trp His Pro
 65 70 75 80
 Gly Thr Gly Ser His Thr Gly Ala Val Arg Arg Arg His Gln Glu Ala
 85 90 95
 Arg Asp Gln Ser Leu Leu Leu Arg Arg Arg Gly Arg Val Asp Leu Asp
 100 105 110
 Gly Gly Gly Arg Leu Arg Arg Val Tyr Arg Phe Gln Gly Cys Leu Val
 115 120 125
 Val Val Phe Gly Gln His Leu Leu Arg Pro Leu Leu Ile Leu Arg Val
 130 135 140
 His Arg Glu Asn Leu Val Ala Gly Arg Arg Val Phe Arg Val Lys Pro
 145 150 155 160
 Phe Glu Pro Asp Tyr Val Phe Ile Ser Arg Met Phe Pro Pro Ser Pro
 165 170 175
 His Val Gln Leu Arg Asp Ile Leu Ser Leu Leu Gly His Arg Ser Ala
 180 185 190
 Gln Phe Gly His Val Glu Tyr Pro Leu Pro Leu Leu Ile Glu Arg Ser
 195 200 205
 Leu Ala Ser Gly Ser Arg Ile Ala Phe Pro Val Val Lys Pro Pro Glu
 210 215 220
 Pro Leu Asp Val Ala Leu Gln Arg Gln Val Glu Ser Val Pro Pro Ile
 225 230 235 240
 Arg Lys Val Arg Glu Arg Cys Ala Leu Val Ala Arg Phe Glu Leu Pro
 245 250 255
 Cys Arg Phe Phe Glu Ile His Glu Val Gly Phe Thr Gly Arg Gly His
 260 265 270
 Pro Arg Arg Ile Gly
 275

(2) INFORMATION FOR SEQ ID NO:186:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:186:

10084843.022502

Arg Val Ala Ala Ser Phe Ile Asp Trp Leu Asp Ser Pro Asp Ser Pro
 1 5 10 15
 Leu Asp Pro Ser Leu Val Ser Ser Leu Leu Asn Ala Val Ser Cys Gly
 20 25 30
 Ala Glu Ser Ser Ala Ser Ser Ser Ala Arg Ser Gly Asn Gly Ser Arg
 35 40 45
 Trp Thr Ser Met Pro Ser Gly Thr Arg Pro Gly Pro Arg Arg Ala Thr
 50 55 60
 Ser Arg Asp Asp Arg Arg Ser Ala Thr Ser Val Ile Pro Ser Arg Arg
 65 70 75 80
 Ser Val Ala Pro Arg Ala Glu Phe Gly Thr Arg Leu Ala Ser His Arg
 85 90 95
 Ala Ser Pro Ser Asn Ala Cys Pro Val Arg Ile Val Thr Ser Ala Ser
 100 105 110
 Gly Arg Pro Ile Ser Ser Pro Pro Ile Val Arg Ser Arg Ser Cys Val
 115 120 125
 Asp Lys Asn Gly Arg Arg Cys Ala Ser Gly Tyr Arg Arg Leu Asn Arg
 130 135 140
 Ala Arg Ser Ser Ser Ile Ala Ala Arg Cys Arg Thr Ile Gly Thr Phe
 145 150 155 160
 Arg Arg Ser Arg Tyr Ser Ala Ser Met Arg Val Ser Thr Asn Ser Pro
 165 170 175
 His Val Thr His Gly Val Ala Pro Gly Val Thr Arg Arg Ile Gly Gly
 180 185 190

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Gln Glu Arg Pro Gln Met Cys Gln Arg Val Ser Glu Ile Glu Pro Arg
 1 5 10 15
 Thr Gln Phe Phe Asn Arg Cys Ala Leu Pro His Tyr Trp His Phe Pro
 20 25 30
 Ala Val Ala Val Phe Ser Lys His Ala Ser Leu Asp Glu Leu Ala Pro

20220.448001

35 40 45
 Arg Asn Pro Arg Arg Ser Ser Arg Arg Asp Ala Glu Asp Arg Arg Val
 50 55 60
 Ile Phe Ala Ala Thr Leu Val Ala Val Asp Pro Pro Leu Arg Gly Ala
 65 70 75 80
 Gly Gly Glu Ala Asp Gln Leu Ile Asp Leu Gly Val Cys Arg Arg Gln
 85 90 95
 Ala Gly Arg Val Arg Arg Gly Gln Glu Leu His His Arg His Arg His
 100 105 110
 Gln Gly Ala Ala Pro Asp Leu Arg Arg Arg Arg Arg His Arg Arg Val
 115 120 125
 Gln Gln His Arg Arg Leu Gln Arg Val Arg Gln Leu Arg Arg Tyr Val
 130 135 140
 Gln Thr Ala His His Arg Arg Phe Ala Arg Thr Asp Arg Val Arg His
 145 150 155 160
 His Val Arg Gly Pro Ser Asn His Arg Arg Arg Val Tyr Arg Gly
 165 170 175
 Arg His Ser Gly Ala Gly Gly Cys Pro Ala Gly Gly Ala Gly Ser Val
 180 185 190
 Gly Gly Ser Ala
 195

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Val Arg Cys Gly Thr Leu Val Pro Val Pro Met Val Glu Phe Leu Thr
 1 5 10 15
 Ser Thr Asn Ala Pro Ser Leu Pro Ser Ala Tyr Ala Glu Val Asp Lys
 20 25 30
 Leu Ile Gly Leu Pro Ala Gly Thr Ala Lys Arg Trp Ile Asn Gly Tyr
 35 40 45
 Glu Arg Gly Gly Lys Asp His Pro Pro Ile Leu Arg Val Thr Pro Gly
 50 55 60
 Ala Thr Pro Trp Val Thr Trp Gly Glu Phe Val Glu Thr Arg Met Leu

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65		70		75		80
Ala Glu Tyr Arg Asp Arg Arg Lys Val Pro Ile Val Arg Gln Arg Ala						
	85			90		95
Ala Ile Glu Glu Leu Arg Ala Arg Phe Asn Leu Arg Tyr Pro Leu Ala						
	100		105			110
His Leu Arg Pro Phe Leu Ser Thr His Glu Arg Asp Leu Thr Met Gly						
	115		120			125
Gly Glu Glu Ile Gly Leu Pro Asp Ala Glu Val Thr Ile Arg Thr Gly						
	130		135			140
Gln Ala Leu Leu Gly Asp Ala Arg Trp Leu Ala Ser Leu Val Pro Asn						
	145		150		155	160
Ser Ala Arg Gly Ala Thr Leu Arg Arg Leu Gly Ile Thr Asp Val Ala						
	165		170			175
Asp Leu Arg Ser Ser Arg Glu Val Ala Arg Arg Gly Pro Gly Arg Val						
	180		185			190
Pro Asp Gly Ile Asp Val His Leu Leu Pro Phe Pro Asp Leu Ala Asp						
	195		200			205
Asp Asp Ala Asp Asp Ser Ala Pro His Glu Thr Ala Phe Lys Arg Leu						
	210		215			220
Leu Thr Asn Asp Gly Ser Asn Gly Glu Ser Gly Glu Ser Ser Gln Ser						
	225		230		235	240
Ile Asn Asp Ala Ala Thr Arg Tyr Met Thr Asp Glu Tyr Arg Gln Phe						
	245		250			255
Pro Thr Arg Asn Gly Ala Gln Arg Ala Leu His Arg Val Val Thr Leu						
	260		265			270
Leu Ala Ala Gly Arg Pro Val Leu Thr His Cys Phe Ala Gly Lys Asp						
	275		280			285
Arg Thr Gly Phe Val Val Ala Leu Val Leu Glu Ala Val Gly Leu Asp						
	290		295			300
Arg Asp Val Ile Val Ala Asp						
	305		310			

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

CTCGTGCCGA TTCGGCACGA GCTGAGCAGC CCAAGGGGCC GTTCGGCGAA GTCATCGAGG	60
CATTGCGCGA CGGGCTGGCC GGCAAGGTA AGCAAATCAA CACCACGCTG AACAGCCTGT	120
CGCAGGCGTT GAACGCCTTG AATGAGGGCC GCGGCGACTT CTTCGCGGTG GTACGCAGCC	180
TGGCGCTATT CGTCAACGCG CTACATCAGG ACGACCAACA GTTCGTCGCG TTGAACAAGA	240
ACCTTGCGGA GTTCACCGAC AGGTTGACCC ACTCCGATGC GGACCTGTG AACGCCATCC	300
AGCAATTCGA CAGCTTGCTC GCCGTCGCGC GCGCGTTCTT CGCCAAGAAC CGCGAGGTGC	360
TGACGCATGA CGTCAATAAT CTCGCGACCG TGACCACCAC GTTGCTGCAG CCCGATCCGT	420
TGGATGGGTT GGAGACCGTC CTGCACATCT TCCCGACGCT GCGCGCGAAC ATTAACCAGC	480
TTTACCATCC GACACACGGT GCGTGGTGT CGCTTTCCGC GTTCACGAAT TTCGCCAACC	540
CGATGGAGTT CATCTGCAGC TCGATTGAG CGGGTAGCCG GCTCGGTTAT CAAGAGTCGG	600
CCGAACCTCT TGCGCAGTAT CTGGCGCCAG TCCTCGATGC GATCAAGTTC AACTACTTTC	660
CGTTCGGCCT GAACGTGGCC AGCACCGCCT CGACACTGCC TAAAGAGATC GCGTACTCCG	720
AGCCCGCCTT GCAGCCGCC AACGGGTACA AGGACACCAC GGTGCCCGGC ATCTGGGTGC	780
CGGATACGCC GTTGTCACAC CGCAACACGC AGCCCGGTTG GGTGGTGGCA CCCGGGATGC	840
AAGGGGTTCA GGTGGGACCG ATCACGCAGG GTTTGCTGAC GCGGAGTCC CTGGCCGAAC	900
TCATGGGTGG TCCCGATATC GCCCTCCGT CGTCAGGGCT GCAAACCCCG CCCGACCCC	960
CGAATGCGTA CGACGAGTAC CCCGTGCTGC CGCCGATCGG TTTACAGGCC CCACAGGTGC	1020
CGATACCACC GCGCCCTCCT GGGCCCGACG TAATCCCGGG TCCGGTGCCA CCGGCTCTGG	1080
CGCGATCGT GTTCCCAAGA GATCGCCCGG CAGCGTCGGA AAAGTTCGAC TACATGGGCC	1140
TCTTGTTGCT GTCGCCGGGC CTGGCGACCT TCCTGTTGCG GGTGTCATCT AGCCCGGCC	1200
GTGGAACGAT GGCCGATCGG CACGTGTTGA TACCGCGCAT CACCGGCGTG GCGTTGATCG	1260
CGGCATTCGT CGCACAATCG TGGTACCGCA CAGAATATCC GCTCATAGAC ATGCGCTTGT	1320
TCCAGAACCAG AGCGGTGCGG CAGGCCAACA TGACGATGAC GGTGCTCTCC CTCGGGCTGT	1380
TTGGCTCCTT CTGTGCTGTC CCGAGCTACC TCCAGCAAGT GTTGACCAAA TCACCGATGC	1440
AATCGGGGGT GCATATCATC CCACAGGGCC TCGGTGCCAT GCTGGCGATG CCGATCGCCG	1500
GAGCGATGAT GGACCGACGG GGACCGGCCA AGATCGTGCT GGTGGGATC ATGCTGATCG	1560
CTGCGGGGTT GGGCACCTTC GCCTTTGGTG TCGCGCGGCA AGCGGACTAC TTACCCATTC	1620

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TGCCGACCGG	GCTGGCAATC	ATGGGCATGG	GCATGGGCTG	CTCCATGATG	CCACTGTCCG	1680
GGCGGCAGT	GCAGACCTG	GCCCCACATC	AGATCGCTCG	CGGTTGCAGC	CTGATCAGCG	1740
TCAACCAGCA	GGTGGGCGGT	TCGATAGGGA	CCGCACTGAT	GTGCGTGCTG	CTCACCTACC	1800
AGTTCAATCA	CAGCGAAATC	ATCGCTACTG	CAAAGAAAGT	CGCACTGACC	CCAGAGAGTG	1860
GCGCCGGGCG	GGGGGCGGCG	GTTGACCTTT	CCTCGCTACC	GCGCCAAACC	AACTTCGCGG	1920
CCCAACTGCT	GCATGACCTT	TCGCACGCCT	ACGCGGTGCT	ATTCGTGATA	GCGACCGCGC	1980
TAGTGGTCTC	GACGCTGATC	CCCGCGGCAT	TCCTGCCGAA	ACAGCAGGCT	AGTCATCGAA	2040
GAGCACCGTT	GCTATCCGCA	TGACGTCTGC	TT			2072

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TCACCCCGGA	GAAGTCGTTT	GTGACGACC	TGGACATCGA	CTCGTGTGCG	ATGTCGAGA	60
TCGCCGTGCA	GACCGAGGAC	AAGTACGGCG	TCAAGATCCC	CGACGAGGAC	CTCGCCGGTC	120
TGCGTACCGT	CGGTGACGTT	GTGCGCTACA	TCCAGAAGCT	CGAGGAAGAA	AACCCGGAGG	180
CGGCTCAGGC	GTTGCGCGCG	AAGATTGAGT	CGGAGAACCC	CGATGCGGCA	CGAGCAGATC	240
GGTGCGTTTC	ACCCACATCG	CAAGCTCGAG	ACGCCCGTGC	TCCTCTTGCA	CGCTCAGCCA	300
GGTTGGCGTG	TCGCCGCTTT	CCAGCAAGTG	TTCCACCAC	ACGAAGGGAC	CCTCGCGAAA	360
GGTGACTGAT	CCGCGGACCA	CATAGTCGAT	GCCACCGTGG	CTGACAATTG	CGCCGGGTCC	420
GAGTTGGCGG	GGGCGGAATT	GCGGCATTGC	GTGGAAGGCC	AGCGGATCCC	GGCGCCCGCC	480
CGCGGTGGCT	GGTGTTTTGG	GCCGCCGGAT	GGCCACGACG	AGAACGACGA	TGCGCGCGAT	540
GAACAGCGCC	ACGGCAATCA	CGACCAGCAG	ATTTCCACAG	CATACCCTCT	CGTACCGCTG	600
CGCCGCGGTT	GGTCGATCGG	TCGCATATCG	ATGGCGCCGT	TTAACGTAAAC	AGCTTTCCGC	660
GGACCGGGGG	TCACAACGGG	CGAGTTGTCC	GGCCGGGAAC	CCGGCAGGCT	TCGGCCCGCG	720
TCACCCGACG	TCAGTGTGTC	ACCATCCGGG	TGTCGGTGAG	CGTGCAACTC	AAACACACTC	780
AACGGCAACG	GTTCCTCAGG	TCACCAGCTC	AACCTCGACC	CGCAATCGCT	CGTACGTTTC	840

GACCGCGCGC AGGTGCGGAG TCAGCAGCTT TGCGCCGGCA GCTTTCGCCG TGAAGCCGAC 900
 CAGGGCATCG TAGGTTGCGC CACCGGTGAC ATCGTGCTCG GCGAGGTGGT CGGTCAAGCC 960
 GCGATATGAG CAGGCATCCA GTGCCAGGTA GTTGCTGGAG GTGATGTCGG CCAAGTAGGC 1020
 GTGGACGGCA ACAGGGGCAA TACGATGCGG CGGTGGTAGC CGGGTCAAGA CCGAATAGGT 1080
 TTCCACAGCC GCGTGCGCGA TCAGATGGAC GCCACGGTTG AGCGCGCGCA CGGCGGCCTC 1140
 GTGCCCTTCG TGCCAGGTGC CGAATCCGGC AACCAGCACG CTGGTGTCTG GTGCGATCAC 1200
 CGCCGTGTGC GATCGAGCGT TTCCGGAACG ATTTGTCGG TCAACGGGGG CAGGGGACGT 1260
 TCTGGCCGTG CGACGAGAAC CGAGCCTTCC CGAACGAGTT CGACACCGGT CGGGGCCGGC 1320
 TCAATCTCGA TGCGCCCATC GCGCTCGGTG ATCTCCACCT GGTGTTCCG CCGCAAGCCA 1380
 AGGCGCTCGC GAATCCGCTT GGGAAATACC AGACGTCTCT CGACATCGAT GGTGTGTCGC 1440
 ATGGTAGGAA ATTTACCATC GCACGTTCCA TAGGCGTGTC CTGCGCGGGA GTGTCGGGACG 1500
 ATCGCTAGC GTATCGAAGC ATTGTTTCGG AAATGGCTGA GGGAGCGTGC GGTGCGGGTG 1560
 ATGGGTGTGC ATCCCGGGTT GACCCGATGC GGGCTGTGCG TCATCGAGAG TGGGCGTGGT 1620
 CGGCAGCTCA CCGCGCTGGA TGTCGACGTG GTGCGCACAC CGTCGGATGC GGCCTTGGCG 1680
 CAGCGCCTGT TGGCCATCAG CGATGCCGTC GAGCACTGGC TGGACACCCA TCATCCGGAG 1740
 GTGTTGGCTA TCGAACGGGT GTTCTCTCAG CTCAACGTGA CCACGGTGAT GGGCACCCGC 1800
 CAGGCCGGCG GCGTGATCGC CTTGGCGGCG GCCAAACGTG GTGTCGACGT GCATTTCAT 1860
 ACCCCAGCGC AGGTCAAGGC GCGGGTCACT GGCAACGGTT CCGCAGACAA GGCTCAGGTC 1920
 ACC 1923

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTGGCGTGCC AGTGTACCGC GCGATATGAC GTGCGCATTC AATTCGCGG CCCGCCGGA 60
 CCCGTCGCCA CCCAATCTGG ACCACCCGGT CGTCAATTG CCGAAGGTCG CCAAGTGCCT 120
 GCCCAATGTG GTGCTGGGTT TCTTGAACGA AGGCCTGCGC TATCGGCTGC CTTACCCCCA 180
 AACACGCCA GTCCAGGAAT CCGGTCCCGC GCGGCCGATT CCCAGCGGCA TCTGCTAGCC 240

GGGGATGGTT CAGACGTAAC GGTGGGCTAG GTCGAAACCC GCGCCAGGGC CGCTGGACGG 300
 GCTCATGGCA GCGAAATTAG AAAACCCGGG ATATTGTCCG CGGATTGTCA TACGATGCTG 360
 AGTGCTTGGT GGTTCGTGTT TAGCCATTGA GTGTGGATGT GTTGAGACCC TGGCCTGGAA 420
 GGGGACAACG TGCTTTTGCC TCTTGGTCCG CTTTGCCCGC CCGACGCGGT GTTGGCGAAA 480
 CGGGCTGAGT CGGGAATGCT CGGCGGGTTG TCGGTTCCGC TCAGCTGGGG AGTGGCTGTG 540
 CCACCCGATG ATTATGACCA CTGGGCGCCT GCGCCGGAGG ACGGCGCCGA TGTCGATGTC 600
 CAGGCGGCCG AAGGGGCGGA CGCAGAGGCC GCGGCCATGG ACGAGTGGGA TGAGTGGCAG 660
 GCGTGGAACG AGTGGGTGGC GGAGAACGCT GAACCCCGCT TTGAGGTGCC ACGGAGTAGC 720
 AGCAGCGTGA TTCCGCATTC TCCGCGCGCC GGCTAGGAGA GGGGGCGCAG ACTGTCGTTA 780
 TTTGACCACT GATCGGCGGT CTCGCTGTTT CCGCGGCCGG CTATGACAAC AGTCAATGTG 840
 CATGACAAGT TACAGGTATT AGGTCCAGGT TCAACAAGGA GACAGGCAAC ATGGCAACAC 900
 GTTTTATGAC GGATCCGCAC GCGATGCGGG ACATGGCGGG CCGTTTGTAG GTGCACGCCC 960
 AGACGCTGGA GGACGAGGCT CGCCGGATGT GGGCGTCCGC GCAAAACATC TCGGGNGCGG 1020
 GCTGGAGTGG CATGCCGAG GCGACCTCGC TAGAC 1055

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CCGCTCTGTT GTTGCATAC TCCGCGCGG CCGCTCGAC CGCACTGGCC GTGGCTGTG 60
 TCCGGCTGA CCACGGGAT CGCCGAACCA TCCGAGATCA CCTCGCAATG ATCCACCTCG 120
 CGCAGTGGT CACCCAGCCA CCGGCGGGT TCGACAGCG CCTGCATCAC CTGTGTATAG 180
 CCGTCGCGCC CCAGCCGCG GAAGTTGTAG TACTGGCCCA CCACCTGGTT ACCGGGACGG 240
 GAGAAGTTCA GGTGAAGGT CGGCATGTCG CCGCCGAGGT AGTTGACCCG GAAAACCA GA 300
 TCCTCGGCA GGTGCTCGG CCCGCGCCAC ACGACAAACC CGACGCGCGG ATAGGTGAC 359

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

AACGGGCCCG TGGGCACCGC TCCTCTAAGG GCTCTCGTTG GTCGCATGAA GTGCTGGAAG      60
GATGCATCTT GGCAGATTCC CGCCAGAGCA AAACAGCCGC TAGTCCTAGT CCGAGTCGCC      120
CGCAAAGTTC CTCGAATAAC TCCGTACCCG GAGCGCCAAA CCGGGTCTCC TTCGCTAAGC      180
TGCGCGAACC ACTTGAGGTT CCGGGACTCC TTGACGTCCA GACCGATTGC TTCGAGTGGC      240
TGATCGGTTT GCGCGCTGG CGCGAATCCG CCGCCGAGCG GGGTGATGTC AACCCAGTGG      300
GTGGCTGGA AGAGGTGCTC TACGAGCTGT CTCGATCGA GGACTTCTCC      350
  
```

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

Glu Gln Pro Lys Gly Pro Phe Gly Glu Val Ile Glu Ala Phe Ala Asp
1           5           10           15
Gly Leu Ala Gly Lys Gly Lys Gln Ile Asn Thr Thr Leu Asn Ser Leu
20          25          30
Ser Gln Ala Leu Asn Ala Leu Asn Glu Gly Arg Gly Asp Phe Phe Ala
35          40          45
Val Val Arg Ser Leu Ala Leu Phe Val Asn Ala Leu His Gln Asp Asp
50          55          60
Gln Gln Phe Val Ala Leu Asn Lys Asn Leu Ala Glu Phe Thr Asp Arg
65          70          75          80
Leu Thr His Ser Asp Ala Asp Leu Ser Asn Ala Ile Gln Gln Phe Asp
85          90          95
Ser Leu Leu Ala Val Ala Arg Pro Phe Phe Ala Lys Asn Arg Glu Val
100         105         110
Leu Thr His Asp Val Asn Asn Leu Ala Thr Val Thr Thr Leu Leu
115         120         125
Gln Pro Asp Pro Leu Asp Gly Leu Glu Thr Val Leu His Ile Phe Pro
130         135         140
  
```

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Thr Leu Ala Ala Asn Ile Asn Gln Leu Tyr His Pro Thr His Gly Gly
 145 150 155 160
 Val Val Ser Leu Ser Ala Phe Thr Asn Phe Ala Asn Pro Met Glu Phe
 165 170 175
 Ile Cys Ser Ser Ile Gln Ala Gly Ser Arg Leu Gly Tyr Gln Glu Ser
 180 185 190
 Ala Glu Leu Cys Ala Gln Tyr Leu Ala Pro Val Leu Asp Ala Ile Lys
 195 200 205
 Phe Asn Tyr Phe Pro Phe Gly Leu Asn Val Ala Ser Thr Ala Ser Thr
 210 215 220
 Leu Pro Lys Glu Ile Ala Tyr Ser Glu Pro Arg Leu Gln Pro Pro Asn
 225 230 235 240
 Gly Tyr Lys Asp Thr Thr Val Pro Gly Ile Trp Val Pro Asp Thr Pro
 245 250 255
 Leu Ser His Arg Asn Thr Gln Pro Gly Trp Val Val Ala Pro Gly Met
 260 265 270
 Gln Gly Val Gln Val Gly Pro Ile Thr Gln Gly Leu Leu Thr Pro Glu
 275 280 285
 Ser Leu Ala Glu Leu Met Gly Gly Pro Asp Ile Ala Pro Pro Ser Ser
 290 295 300
 Gly Leu Gln Thr Pro Pro Gly Pro Pro Asn Ala Tyr Asp Glu Tyr Pro
 305 310 315
 Val Leu Pro Pro Ile Gly Leu Gln Ala Pro Gln Val Pro Ile Pro Pro
 325 330 335
 Pro Pro Pro Gly Pro Asp Val Ile Pro Gly Pro Val Pro Pro Val Leu
 340 345 350
 Ala Ala Ile Val Phe Pro Arg Asp Arg Pro Ala Ala Ser Glu Asn Phe
 355 360 365
 Asp Tyr Met Gly Leu Leu Leu Ser Pro Gly Leu Ala Thr Phe Leu
 370 375 380
 Phe Gly Val Ser Ser Ser Pro Ala Arg Gly Thr Met Ala Asp Arg His
 385 390 395 400
 Val Leu Ile Pro Ala Ile Thr Gly Leu Ala Leu Ile Ala Ala Phe Val
 405 410 415
 Ala His Ser Trp Tyr Arg Thr Glu His Pro Leu Ile Asp Met Arg Leu
 420 425 430
 Phe Gln Asn Arg Ala Val Ala Gln Ala Asn Met Thr Met Thr Val Leu

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435 440 445
 Ser Leu Gly Leu Phe Gly Ser Phe Leu Leu Leu Pro Ser Tyr Leu Gln
 450 455 460
 Gln Val Leu His Gln Ser Pro Met Gln Ser Gly Val His Ile Ile Pro
 465 470 475 480
 Gln Gly Leu Gly Ala Met Leu Ala Met Pro Ile Ala Gly Ala Met Met
 485 490 495
 Asp Arg Arg Gly Pro Ala Lys Ile Val Leu Val Gly Ile Met Leu Ile
 500 505 510
 Ala Ala Gly Leu Gly Thr Phe Ala Phe Gly Val Ala Arg Gln Ala Asp
 515 520 525
 Tyr Leu Pro Ile Leu Pro Thr Gly Leu Ala Ile Met Gly Met Gly Met
 530 535 540
 Gly Cys Ser Met Met Pro Leu Ser Gly Ala Ala Val Gln Thr Leu Ala
 545 550 555 560
 Pro His Gln Ile Ala Arg Gly Ser Thr Leu Ile Ser Val Asn Gln Gln
 565 570 575
 Val Gly Gly Ser Ile Gly Thr Ala Leu Met Ser Val Leu Leu Thr Tyr
 580 585 590
 Gln Phe Asn His Ser Glu Ile Ile Ala Thr Ala Lys Lys Val Ala Leu
 595 600 605
 Thr Pro Glu Ser Gly Ala Gly Arg Gly Ala Ala Val Asp Pro Ser Ser
 610 615 620
 Leu Pro Arg Gln Thr Asn Phe Ala Ala Gln Leu Leu His Asp Leu Ser
 625 630 635
 His Ala Tyr Ala Val Val Phe Val Ile Ala Thr Ala Leu Val Val Ser
 645 650 655
 Thr Leu Ile Pro Ala Ala Phe Leu Pro Lys Gln Gln Ala Ser His Arg
 660 665 670
 Arg Ala Pro Leu Leu Ser Ala
 675

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Thr Pro Glu Lys Ser Phe Val Asp Asp Leu Asp Ile Asp Ser Leu Ser
 1 5 10 15

Met Val Glu Ile Ala Val Gln Thr Glu Asp Lys Tyr Gly Val Lys Ile
 20 25 30

Pro Asp Glu Asp Leu Ala Gly Leu Arg Thr Val Gly Asp Val Val Ala
 35 40 45

Tyr Ile Gln Lys Leu Glu Glu Asn Pro Glu Ala Ala Gln Ala Leu
 50 55 60

Arg Ala Lys Ile Glu Ser Glu Asn Pro Asp Ala Ala Arg Ala Asp Arg
 65 70 75 80

Cys Val Ser Pro Thr Ser Gln Ala Arg Asp Ala Arg Arg Pro Leu Ala
 85 90 95

Arg Ser Ala Arg Leu Ala Cys Arg Arg Leu Pro Ala Ser Val Pro Thr
 100 105 110

Thr Arg Arg Asp Pro Arg Glu Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Leu Ala Cys Gln Cys His Arg Arg Tyr Asp Val Gly Ile Gln Phe Arg
 1 5 10 15

Gly Pro Ala Gly Pro Val Ala Thr Gln Ser Gly Pro Pro Gly Pro Ser
 20 25 30

Ile Ala Glu Gly Arg Gln Val Arg Ala Gln Cys Gly Ala Gly Phe Leu
 35 40 45

Glu Arg Arg Pro Ala Val Ser Gly Ala Leu Pro Pro Asn Asn Ala Ser
 50 55 60

Pro Gly Ile Arg Ser Arg Ala Ala Asp Ser Gln Arg His Leu Leu Ala
 65 70 75 80

Gly Asp Gly Ser Asp Val Thr Val Gly
 85

(2) INFORMATION FOR SEQ ID NO:197:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

Ala Ser Leu Leu Ala Tyr Ser Ala Ala Ala Ser Thr Ala Leu Ala
1           5           10           15

Val Ala Cys Val Arg Ala Asp His Arg Asp Arg Arg Thr Ile Arg Asp
          20           25           30

His Leu Ala Met Ile His Leu Ala Gln Leu Val Thr Gln Pro Pro Gly
          35           40           45

Gly Val Arg Gln Arg Leu His His Leu Gly Ile Ala Val Ala Pro Gln
          50           55           60

Pro Gln Glu Val Val Val Leu Ala His His Leu Val Thr Gly Thr Gly
          65           70           75           80

Glu Val Gln Gly Glu Gly Arg His Val Ala Ala Glu Val Val Asp Pro
          85           90           95

Glu Asn Gln Ile Leu Arg Gln Val Leu Gly Pro Ala Pro His Asp Lys
          100          105          110

Pro Asp Ala Gly Ile Gly Gln
          115
  
```

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```

Arg Ala Arg Gly His Arg Ser Ser Lys Gly Ser Arg Trp Ser His Glu
1           5           10           15

Val Leu Glu Gly Cys Ile Leu Ala Asp Ser Arg Gln Ser Lys Thr Ala
          20           25           30

Ala Ser Pro Ser Pro Ser Arg Pro Gln Ser Ser Ser Asn Asn Ser Val
          35           40           45

Pro Gly Ala Pro Asn Arg Val Ser Phe Ala Lys Leu Arg Glu Pro Leu
          50           55           60
  
```

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Glu Val Pro Gly Leu Leu Asp Val Gln Thr Asp Ser Phe Glu Trp Leu
65 70 75 80

Ile Gly Ser Pro Arg Trp Arg Glu Ser Ala Ala Glu Arg Gly Asp Val
85 90 95

Asn Pro Val Gly Gly Leu Glu Glu Val Leu Tyr Glu Leu Ser Pro Ile
100 105 110

Glu Asp Phe Ser
115

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

TGCTACGCAG CAATCGCTTT GGTGACAGAT GTGGATGCCG GCCTCGCTGC TGGCGATGGC	60
GTGAAAGCCG CCGACGTGTT CGCCGCATTC GGGGAGAACA TCGAACTGCT CAAAAGGCTG	120
GTGCGGGCCG CCATCGATCG GGTGCGCCGAC GAGCGCACGT GCACGCACTG TCAACACCAC	180
GCCGGTGTTT CGTTGCCGTT CGAGCTGCCA TGAGGGTGCT GCTGACCCGC GCGGCCGGCT	240
TCATCGGGTC GCGCGTGGAT GCGGCGTTAC GGGCTGCGGG TCACGACGTG GTGGGCGTCG	300
ACGCGCTGCT GCCCGCCGCG CACGGGCCAA ACCCGGTGCT GCCACCGGGC TGCCAGCGGG	360
TCGACGTGCG CGACGCCAGC GCGCTGGCCC CGTTGTTGGC CGTGTCGATG CTGGTGTGTC	420
ACCAGGCCGC CATGTTGGGT GCCGGCGTCA ACGCCGCCGA CGCACCCGCC TATGGCGGCC	480
ACAACGATTT CGCCACCACG GTGCTGCTGG CGCAGATGTT CGCCCGCGGG GTCCGCCGTT	540
TGGTGCTGGC GTCGTCGATG GTGGTTTACG GGCAGGGGCG CTATGACTGT CCGCAGCATG	600
GACCGGTGCA CCCGCTGCCG CGGCGGCGAG CCGACCTGGA CAATGGGGTC TTCGAGCACC	660
GTGCCCCGGG GTGCGGCGAG CCAGTCATCT GGCAATGGT CGACGAAGAT GCCCGTGTGC	720
GCCCCGCGAG CCGTGTACGCG GCAGCAAGAC CGCGCAGGAG CACTACGCGC TGGCGTGGTC	780
GGAAACGAAT GCGCGTTCGG TGGTGGCGTT G	811

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GTCCCGCGAT GTGCCCGAGC ATGACTTTTCG GCAACACCGG CGTAGTAGTC GAAGATATCG	60
GACTTTGTGG TCCCGGTGGC GGGATAGAGC ACCTGTGCGC GTTGGTCAGC GTCACCCGTT	120
GCTCGGACGC CGAACCCATG CTTTCAACGT AGCCTGTCGG TCACACAAGT CGCGAGCGTA	180
ACGTCACGGT CAAATATCGC GTGGAATTTC GCCGTGACGT TCCGCTCGCG GACAATCAAG	240
GCATACTCAC TTACATGCGA GCCATTGGA CGGGTTCGAT CGCCTTCGGG CTGGTGAACG	300
TGCCCGTCAA GGTGTACAGC GCTACCGCAG ACCACGACAT CAGGTTCCAC CAGGTGCACG	360
CCAAGGACAA CGGACGCATC CGGTACAAGC GCGTCTGCGA GCGGTGTGGC GAGGTGGTCG	420
ACTACCGCGA TCTTGCCCGC GCCTACGAGT CGGCGCAGCG CCAATGGTG GCGATCACCG	480
ACGACGACAT CGCAGCTTG CCTGAAGAAC GCAGCCGGGA GATCGAGGTG TTGGAGTTTG	540
TCCCGCCCGC CGACGTGGAC CCGATGATGT TCGACCGCAG CTACTTTTTG GAGCCTGATT	600
CGAAGTCGTC GAAATCGTAT GTGCTGTGG CTAAGACACT CGCCGAGACC GACCGGATGG	660
CGATCGTGGA TCGCCCCACC GGCGTGAAT GCAGGAAAAA TAAGAGCCGC TATCCACAAT	720
TCGGCGTCGA GCTCGGCTAC CACAAACGGT AGAACGATCG AGACATTCCC GAGCTGAAGT	780
GCGGCGCTAT AGAAGCCGCT CTGCGCGATT ATCAAACGCA AAATACGCTT ACTCATGCCA	840
TCGGCGCTGC TCACCCGATG CGACGTTTTT GCCACGCTCC ACCGCCTGCC GCGCGACCTC	900
AAGTGGGCAT GCATCCCACC CGTTCCCGGA AACCAGTTCC GCGGGGTCGG CTCATCGCTT	960
CATCCT	966

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CCGCACCGCC GGCAATACCG CCAGCGCCAC CGTTACCGCC GTTGGCGCCG TTGCCCCCGT	60
TGCCGCCCGT CCCGCCGCC CCGCCGATGG AGTTCTCATC GCCAAAAGTA CTGGCGTTGC	120
CACCGGAGCC GCCGTTGCCG CGTCCACGC CAGCCCCGCC GACTCCACCG GCCCCACCGA	180

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CTCCGCCGCT GCCACCGTTG CCGCCGTTGC CGATCAACAT GCCGCTGGCG CCACCCTTGC	240
CACCCACGCC ACCGGCTCCG CCCACCCCGC CGACACCAAG CGAGCTGCCG CCGGAGCCAC	300
CATCACCACC TACGCCACCG ACCGCCCAGA CACCAGCGAC CGGGTCTTCG TGAACGTCG	360
CGGTGCCACC ACCGCCCGCG TTACCGCCAA CCCCACCGGC AACGCCGGCG CCGCCATCCC	420
CGCCGGCCCC GCGGTTGGCG CCGTTGCCGC CGTTGCCGAA CAACAACCCG CCGCGCGCCG	480
CGTTGCCGCC CGCGCCCGCG GTCCCGCCGG CGCCGCGGAC GCCAAGGCGG CTGCCGCCCT	540
TGCCGCCATC ACCACCCCTG CCGCCGACCA CATCGGGTTC TGCCCTGGGG TCTGGGCTGT	600
CAAACTCTGC GATGCCAGCG TTGCCGCCGC TTCCCCGGG CCCCCCGTG GCGCCGTAC	660
CACCGATACC ACCCGCGCCA CCGCGCCAC CGTTGCCGCC ATCACCGAAT AGCAACCCGC	720
CGCGCCACC ATTGCCGCC GCTCCCCCTG CGCCACCGTC GCGCGCGGAG GCGGCACTGG	780
CAGCCCCGTT ACCACCGAAA CCGCGCTAC CACCGTAGA GGTGGCAGTG GCGATGTGTA	840
CGAAAGCGCC GCCTCCGGCG CCGCGCTAC CACCCCCACT GCGCGCGGCT ACACCGTCGG	900
ACCCGTTGCC ACCATCACCG CCAAAGGCGC TCGCAATGTC GCCCTCGCG ACTCCGCGT	960
CGCCGCCGTT GCGCGCCCGC CCACCGGCG CGGCGGTACC GCCGTACCA CCGGCACCGC	1020
CGGTGGCCTT GCCCGAGCCT GCCGTGCGG TGGCACCCTG GCGCGCGGTG CCACCGGTG	1080
GCGTGCCGGC AGTGCCATGG CCGCCCGTGC CGCCGTGCGC GCGGTTTGA TCACCGATGC	1140
CGGACATATC TGCCGGGCTG TCCCGGTGC TGGCCGCGGG GCGGGCGGTG GGATTGACCC	1200
CGTTTGCCCC GCGGAGGCGG GCGCGGCCGG TACCACCGGC GCGGCCATGG CCGAACAGCC	1260
GCGCGTTGCC GCGGTTACCG CCGCACCCC CGATGCTGCG GCGCACGTG GTGCCGCCGA	1320
CACCGCGGTT GCGCGCGTTG CCCACAACC ACCCCCCGTT CCCACCGCA CCGCGGCGG	1380
GCGCGGTACC ACCGGCCCCG CGGTTGCCGC CGTTGCCGAT CAACCCGGCC GCGCCTCCGC	1440
TGCCCGCGGT TTGACCGAAC CCGCCAGCG CGCGTTGCC ACCGTTGCCA AACAGCAACC	1500
GCGCGGCGCG GCCAGGCTGC CCGGCTGCC TCCGCTCGG GCGGTTTCC ATCAACGGG	1560
GCCCCAAAAG CGCCTCGGTG GCGCATTTCA CCGCACCGAG CAGACTCCG TCAACAGCGG	1620
CTTCAGTGCT GGCATACCGA CCGCGGGCG CAGTCAACGC CTGCACAAAC TGCTCGTGAA	1680
ACGCTGCCAC CTGTACGCTG AGCGCTGAT ACTGCCGAGC ATGGGCCCCG AACAAACCCG	1740
CAATCGCCGC CGACACTTCA TCGGCAGCG CAGCCACCAC TTCGTCGTC GGGATCGCCG	1800
CGGCCGCAAT AGCCGCGCTC ACCTGCGAAC CAATAGTCGA TAAATCAAA CCGCGAGTTG	1860

CCAGCAGCTG CGGCGTCGCG ATCACCAAGG ACACCTCGCA CCTCCGGATA CCCCATATCG 1920
 CCGCACCCTG TCCCCAGCGG CCACGTGACC TTTGGTCGCT GGCTGGCGGC CCTGACTATG 1980
 GCGCGGACGG CCTTCGTCTT GATTGCGCCC GCGCGCGCAG TTGTTGCGCG AGTTGAAGAC 2040
 GGGAGGACAG GCCGAGCTTG GTGTAGACGT GGGTCAAGTG GGAATGCACG GTCCGCGCGC 2100
 AGATGAATAG GCGGACGCGG ATCTCCTTGT TGCTGAGTCC CTCACCGACC AGTAGAGCCA 2160
 CCTCAAGCTC TGTCGGTGTC AACCGGCCCC AGCCACTTGT CGGGCGTTTC CGTGACCGCG 2220
 GGCTCGTTG CGCGTACGCG ATCGCCTCAT CGATCGATAA CGCAGTTCCT TCGGCCCAGG 2280
 CATCGTCGAA CTCGCTGTCA CCCATGGATT TTCGAAGGGT GGCTAGCGAC GAGTTACAGC 2340
 CCGCCTGGTA GATCCCGAAG CGGACCG 2367

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gln Pro Ala Gly Ala Thr Ile Ala Ala Ser Ser Pro Cys Ala Thr Val
 1 5 10 15
 Gly Ala Gly Gly Gly Thr Gly Ser Pro Val Thr Thr Glu Thr Ala Ala
 20 25 30
 Thr Thr Gly Arg Gly Gly Ser Gly Asp Val Tyr Glu Ser Ala Ala Ser
 35 40 45
 Gly Ala Ala Ala Thr Thr Pro Thr Ala Gly Gly Tyr Thr Val Gly Pro
 50 55 60
 Val Ala Thr Ile Thr Ala Lys Gly Ala Arg Asn Val Ala Leu Arg Asp
 65 70 75 80
 Ser Ala Val Ala Ala Val Ala Ala Ala Thr Gly Ser Gly Gly Thr
 85 90 95
 Ala Val Thr Thr Gly Thr Ala Gly Gly Leu Ala Arg Ala Cys Arg Arg
 100 105 110
 Gly Gly Thr Val Ala Ala Gly Ala Thr Gly Arg Arg Ala Gly Ser Ala
 115 120 125
 Met Ala Ala Arg Ala Ala Val Ala Ala Gly Leu Ile Thr Asp Ala Gly
 130 135 140

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His Ile Cys Arg Ala Val Pro Gly Ala Gly Arg Gly Ala Gly Arg Gly
 145 150 155 160
 Ile Asp Pro Val Cys Pro Gly Glu Ala Gly Ala Gly Thr Thr Gly
 165 170 175
 Ala Ala Met Ala Glu Gln Pro Gly Val Ala Ala Val Thr Ala Arg Thr
 180 185 190
 Pro Asp Ala Cys Gly His Ala Gly Ala Ala Asp Thr Ala Val Ala Ala
 195 200 205
 Val Ala Pro Gln Pro Pro Pro Val Pro Thr Gly Thr Ala Gly Arg Ala
 210 215 220
 Gly Thr Thr Gly Pro Ala Val Ala Val Ala Asp Gln Pro Gly Arg
 225 230 235 240
 Ala Ser Ala Ala Ala Gly Leu Thr Glu Pro Ala Ser Arg Ala Val Ala
 245 250 255
 Thr Val Ala Lys Gln Gln Pro Ala Gly Arg Ala Arg Leu Pro Gly Cys
 260 265 270
 Arg Pro Val Gly Ala Val Ser Asp Gln Arg Ala Pro Gln Lys Arg Leu
 275 280 285
 Gly Gly Arg Ile His Arg Thr Gln Gln Thr Pro Leu Asn Ser Gly Phe
 290 295 300
 Ser Ala Gly Ile Pro Thr Arg Gly Arg Ser Gln Arg Leu His Lys Leu
 305 310 315 320
 Leu Val Lys Arg Cys His Leu Tyr Ala Glu Arg Leu Ile Leu Pro Ser
 325 330 335
 Met Gly Pro Glu Gln Pro Arg Asn Arg Arg Arg His Phe Ile Gly Ser
 340 345 350
 Arg Ser His His Phe Arg Arg Arg Asp Arg Arg Gly Arg Ile Ser Arg
 355 360 365
 Ala His Leu Arg Thr Asn Ser Arg
 370 375

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2852 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

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GGCCAAACG CCCGCGCAT CGCGCCACC GAGGCCGCT ACGACCAGAT GTGGGCCAG	60
GACGTGGCGG CGATGTTTGG CTACCATGCC GGGGCTTCGG CGGCCGTCTC GGCCTTGACA	120
CCGTTGCGCC AGGCGCTGCC GACCGTGCGG GCGGCGGGT CGCTGGTCAG CGCGGCCGCG	180
GCTCAGTGTA CCACGCGGGT CTTCGCAAC CTGGGCTTGG CGAACGTCCG CGAGGGCAAC	240
GTCCGCAACG GTAATGTCCG GAACCTCAAT CTCGGCTCGG CCAACATCGG CAACGGCAAC	300
ATCGGCAGCG GCAACATCGG CAGCTCCAAC ATCGGGTTTG GCAACGTGGG TCCTGGGTTG	360
ACCGCAGCGC TGAACAACAT CGGTTTCGGC AACACCGGCA GCAACAACAT CGGGTTTGCC	420
AACACCGGCA GCAACAACAT CGGGTTCGGC AATACCGGAG ACGGCAACCG AGGTATCGGG	480
CTCACGGGTA GCGGTTTGTG GGGGTTTCGGC GGCCTGAACT CGGGCACCAG CAACATCGGT	540
CTGTTCAACT CGGSCACCGG AAACGTCGGC ATCGSAACT CGGGTACCGG GAACTGGGCG	600
ATTGGCAACT CGGGCAACAG CTACAACACC GGTTTTGCCA ACTCCGGCGA CGCCAACACG	660
GGCTTCTTCA ACTCCGGAAT AGCCAACACC GGCCTCGGCA ACGCCGCGCA CTACAACACC	720
GGTAGCTACA ACCCGGGCAA CAGCAATACC GCGGCTTCA ACATGGGCCA GTACAACACG	780
GGCTACCTGA ACAGCGGCAA CTACAACACC GGGTTGGCAA ACTCCGGCAA TGTCAACACC	840
GGCGCCTTCA TTA CTGGCAA CTTCAACAA GGCCTTCTGT GCGCGCGCA CCACCAAGGC	900
CTGATTTTCG GGAGCCCCG CTCTTCAAC TCGACCACTG CGCGTCGTC GGGATTCTTC	960
AACAGCGGTG CCGGTAGCGC GTCGGCTTC CTGAACCTCG GTGCCAACAA TTCTGGCTTC	1020
TTCAACTCTT CGTCGGGGC CATCGGTAAC TCCGGCCTGG CAAACGCGGG CGTGCTGGTA	1080
TCGGGCGTGA TCAACTCGGG CAACACCGTA TCGGGTTTGT TCAACATGAG CCTGGTGGCC	1140
ATCACAACGC CGGCCTTGAT CTCGGCTTC TTCAACACCG GAAGCAACAT GTCGGGATT	1200
TTCCGTGGCC CACCGGTCTT CAATCTCGGC CTGGCAAACC GGGCGCTCGT GAACATTCTC	1260
GGCAACGCCA ACATCGGCAA TTACAACATT CTCGGCAGCG GAAACGTCGG TGACTTCAAC	1320
ATCCTTGGCA GCGGCAACCT CGGCAGCCAA AACATCTTGG GCAGCGGCAA CGTCGGCAGC	1380
TTCAATATCG GCAGTGAAAA CATCGGAGTA TTCAATGTGC GTTCGGGAAG CCTGGGAAAC	1440
TACAACATCG GATCCGAAA CCTCGGGATC TACAACATCG GTTTTGAAA CGTCGGCGAC	1500
TACAACGTGC GCTTCGGGAA CGCGGGCGAC TTCAACCAAG GCTTTGCAA CACCGGCAAC	1560
AACAACATCG GGTTCGCCAA CACCGGCAAC AACAACATCG GCATCGGGCT GTCCGGCGAC	1620

AACCAGCAGG GCTTCAATAT TGCTAGCGGC TGGAACTCGG GCACCGGCAA CAGCGGCCTG 1680
 TTCAATTCGG GCACCAATAA CGTTGGCATC TTCAACGCGG GCACCGGAAA CGTCGGCATC 1740
 GCAAACCTCGG GCACCGGGAA CTGGGGTATC GGGAAACCCG GTACCGACAA TACCGGCATC 1800
 CTCAATGCTG GCAGCTACAA CACGGGCATC CTCAACGCCG GCGACTTCAA CACGGGCTTC 1860
 TACAACACGG GCAGCTACAA CACGGGCGC TTCAACGTCG GTAACACCAA CACCGGCAAC 1920
 TTCAACGTGG GTGACACCAA TACCGGCAGC TATAACCCGG GTGACACCAA CACCGGCTTC 1980
 TTCAATCCCG GCAACGTCAA TACCGGCGCT TTCGACACGG GCGACTTCAA CAATGGCTTC 2040
 TTGGTGGCGG GCGATAACCA GGGCCAGATT GCCATCGATC TCTCGGTCAC CACTCCATT 2100
 ATCCCATAA ACGAGCAGAT GGTCAATTGAC GTACACAACG TAATGACCTT CGGCGGCAAC 2160
 ATGATCACGG TCACCGAGGC CTCGACCGTT TTCCCCCAA CCTTCTATCT GAGCGGTTTG 2220
 TTCTTCTTCG GCCCGGTCAA TCTCAGCGCA TCCACGCTGA CCGTTCGAC GATCACCTC 2280
 ACCATCGGCG GACCGACGGT GACCGTCCCC ATCAGCATTG TCGGTGCTCT GGAGAGCCGC 2340
 ACGATTACCT TCTCAAGAT CGATCCGGCG CCGGGCATCG GAAATTCGAC CACCAACCCC 2400
 TCGTCCGGCT TCTTCAACTC GGGCACCGGT GGCACATCTG GCTTCCAAA CGTCGGCGGC 2460
 GGCAGTTCAG GCGTCTGGAA CAGTGGTTTG AGCAGCGCGA TAGGGAATTC GGGTTTCAG 2520
 AACCTCGGCT CGCTGCAGTC AGGCTGGGCG AACCTGGGCA ACTCCGTATC GGGCTTTTTC 2580
 AACACCAGTA CGGTGAACCT CTCCACGCCG GCCAATGTCT CGGSCCTGAA CAACATCGGC 2640
 ACCAACCTGT CCGCGGTGTT CCGCGGTCCG ACCGGGACGA TTTTCAACGC GGGCTTTGCC 2700
 AACCTGGGCC AGTTGAACAT CGGCAGCGCC TCGTGCGGAA TTCGGCACGA GTTAGATACG 2760
 GTTTCACAA TCATATCCGC GTTTTGGGCG AGTGCACTAG ACGAATCGAA CCGGGAAGC 2820
 GTAAGCGAAT AAACCGAATG GCGGCCTGTC AT 2852

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gly Gln Asn Ala Pro Ala Ile Ala Ala Thr Glu Ala Ala Tyr Asp Gln
 1 5 10 15

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Met Trp Ala Gln Asp Val Ala Ala Met Phe Gly Tyr His Ala Gly Ala
 20 25 30
 Ser Ala Ala Val Ser Ala Leu Thr Pro Phe Gly Gln Ala Leu Pro Thr
 35 40 45
 Val Ala Gly Gly Gly Ala Leu Val Ser Ala Ala Ala Gln Val Thr
 50 55 60
 Thr Arg Val Phe Arg Asn Leu Gly Leu Ala Asn Val Arg Glu Gly Asn
 65 70 75 80
 Val Arg Asn Gly Asn Val Arg Asn Phe Asn Leu Gly Ser Ala Asn Ile
 85 90 95
 Gly Asn Gly Asn Ile Gly Ser Gly Asn Ile Gly Ser Ser Asn Ile Gly
 100 105 110
 Phe Gly Asn Val Gly Pro Gly Leu Thr Ala Ala Leu Asn Asn Ile Gly
 115 120 125
 Phe Gly Asn Thr Gly Ser Asn Asn Ile Gly Phe Gly Asn Thr Gly Ser
 130 135 140
 Asn Asn Ile Gly Phe Gly Asn Thr Gly Asp Gly Asn Arg Gly Ile Gly
 145 150 155 160
 Leu Thr Gly Ser Gly Leu Leu Gly Phe Gly Gly Leu Asn Ser Gly Thr
 165 170 175
 Gly Asn Ile Gly Leu Phe Asn Ser Gly Thr Gly Asn Val Gly Ile Gly
 180 185 190
 Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn Ser Gly Asn Ser Tyr
 195 200 205
 Asn Thr Gly Phe Gly Asn Ser Gly Asp Ala Asn Thr Gly Phe Phe Asn
 210 215 220
 Ser Gly Ile Ala Asn Thr Gly Val Gly Asn Ala Gly Asn Tyr Asn Thr
 225 230 235 240
 Gly Ser Tyr Asn Pro Gly Asn Ser Asn Thr Gly Gly Phe Asn Met Gly
 245 250 255
 Gln Tyr Asn Thr Gly Tyr Leu Asn Ser Gly Asn Tyr Asn Thr Gly Leu
 260 265 270
 Ala Asn Ser Gly Asn Val Asn Thr Gly Ala Phe Ile Thr Gly Asn Phe
 275 280 285
 Asn Asn Gly Phe Leu Trp Arg Gly Asp His Gln Gly Leu Ile Phe Gly
 290 295 300
 Ser Pro Gly Phe Phe Asn Ser Thr Ser Ala Pro Ser Ser Gly Phe Phe

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305		310		315		320
Asn Ser Gly Ala Gly Ser Ala Ser Gly Phe Leu Asn Ser Gly Ala Asn						
	325			330		335
Asn Ser Gly Phe Phe Asn Ser Ser Ser Gly Ala Ile-Gly Asn Ser Gly						
	340			345		350
Leu Ala Asn Ala Gly Val Leu Val Ser Gly Val Ile Asn Ser Gly Asn						
	355			360		365
Thr Val Ser Gly Leu Phe Asn Met Ser Leu Val Ala Ile Thr Thr Pro						
	370			375		380
Ala Leu Ile Ser Gly Phe Phe Asn Thr Gly Ser Asn Met Ser Gly Phe						
	385			390		395
Phe Gly Gly Pro Pro Val Phe Asn Leu Gly Leu Ala Asn Arg Gly Val						
				405		410
						415
Val Asn Ile Leu Gly Asn Ala Asn Ile Gly Asn Tyr Asn Ile Leu Gly						
				420		425
						430
Ser Gly Asn Val Gly Asp Phe Asn Ile Leu Gly Ser Gly Asn Leu Gly						
				435		440
						445
Ser Gln Asn Ile Leu Gly Ser Gly Asn Val Gly Ser Phe Asn Ile Gly						
				450		455
						460
Ser Gly Asn Ile Gly Val Phe Asn Val Gly Ser Gly Ser Leu Gly Asn						
				465		470
						475
						480
Tyr Asn Ile Gly Ser Gly Asn Leu Gly Ile Tyr Asn Ile Gly Phe Gly						
				485		490
						495
Asn Val Gly Asp Tyr Asn Val Gly Phe Gly Asn Ala Gly Asp Phe Asn						
				500		505
						510
Gln Gly Phe Ala Asn Thr Gly Asn Asn Asn Ile Gly Phe Ala Asn Thr						
				515		520
						525
Gly Asn Asn Asn Ile Gly Ile Gly Leu Ser Gly Asp Asn Gln Gln Gly						
				530		535
						540
Phe Asn Ile Ala Ser Gly Trp Asn Ser Gly Thr Gly Asn Ser Gly Leu						
				545		550
						555
						560
Phe Asn Ser Gly Thr Asn Asn Val Gly Ile Phe Asn Ala Gly Thr Gly						
				565		570
						575
Asn Val Gly Ile Ala Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn						
				580		585
						590
Pro Gly Thr Asp Asn Thr Gly Ile Leu Asn Ala Gly Ser Tyr Asn Thr						
				595		600
						605

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Gly Ile Leu Asn Ala Gly Asp Phe Asn Thr Gly Phe Tyr Asn Thr Gly
 610 615 620
 Ser Tyr Asn Thr Gly Gly Phe Asn Val Gly Asn Thr Asn Thr Gly Asn
 625 630 635 640
 Phe Asn Val Gly Asp Thr Asn Thr Gly Ser Tyr Asn Pro Gly Asp Thr
 645 650 655
 Asn Thr Gly Phe Phe Asn Pro Gly Asn Val Asn Thr Gly Ala Phe Asp
 660 665 670
 Thr Gly Asp Phe Asn Asn Gly Phe Leu Val Ala Gly Asp Asn Gln Gly
 675 680 685
 Gln Ile Ala Ile Asp Leu Ser Val Thr Thr Pro Phe Ile Pro Ile Asn
 690 695 700
 Glu Gln Met Val Ile Asp Val His Asn Val Met Thr Phe Gly Gly Asn
 705 710 715 720
 Met Ile Thr Val Thr Glu Ala Ser Thr Val Phe Pro Gln Thr Phe Tyr
 725 730 735
 Leu Ser Gly Leu Phe Phe Phe Gly Pro Val Asn Leu Ser Ala Ser Thr
 740 745 750
 Leu Thr Val Pro Thr Ile Thr Leu Thr Ile Gly Gly Pro Thr Val Thr
 755 760 765
 Val Pro Ile Ser Ile Val Gly Ala Leu Glu Ser Arg Thr Ile Thr Phe
 770 775 780
 Leu Lys Ile Asp Pro Ala Pro Gly Ile Gly Asn Ser Thr Thr Asn Pro
 785 790 795 800
 Ser Ser Gly Phe Phe Asn Ser Gly Thr Gly Gly Thr Ser Gly Phe Gln
 805 810 815
 Asn Val Gly Gly Gly Ser Ser Gly Val Trp Asn Ser Gly Leu Ser Ser
 820 825 830
 Ala Ile Gly Asn Ser Gly Phe Gln Asn Leu Gly Ser Leu Gln Ser Gly
 835 840 845
 Trp Ala Asn Leu Gly Asn Ser Val Ser Gly Phe Phe Asn Thr Ser Thr
 850 855 860
 Val Asn Leu Ser Thr Pro Ala Asn Val Ser Gly Leu Asn Asn Ile Gly
 865 870 875 880
 Thr Asn Leu Ser Gly Val Phe Arg Gly Pro Thr Gly Thr Ile Phe Asn
 885 890 895

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Ala Gly Leu Ala Asn Leu Gly Gln Leu Asn Ile Gly Ser Ala Ser Cys
 900 905 910

Arg Ile Arg His Glu Leu Asp Thr Val Ser Thr Ile Ile Ser Ala Phe
 915 920 925

Cys Gly Ser Ala Ser Asp Glu Ser Asn Pro Gly Ser Val Ser Glu
 930 935 940

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC 53

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA 42

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T 31

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

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CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GGATATCTGC AGAATTCAGG TTAAAGCCC ATTGCGA

38

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CCGCATGCGA GCCACGTGCC CACAACGGCC

30

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CTTCATGGAA TTCTCAGGCC GGTAAAGTCC GCTGCGG

37

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7676 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

TGGCGAATGG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG TGGTTACGCG	60
CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCCGCT CTTTCGCTT TCTTCCCTTC	120
CTTTCGCGCC ACGTTCGCGG GCTTTCGCG TCAAGCTCTA AATCGGGGCG TCCCTTTAGG	180
GTTCCGATT AGTGCTTTAC GGCACCTCGA CCCCAAAAA CTTGATTAGG GTGATGGTTC	240
ACGTAGTGGG CCATCGCCCT GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT	300
CTTTAATAGT GGACTCTTGT TCCAACTGG AACCAACTC AACCTATCT CGGTCATATC	360
TTTTGATTTA TAAGGGGATT TGCCGATTTC GGCCTATTGG TAAAAAATG AGCTGATTTA	420
ACAAAAATTT AACGCGAATT TTAACAAAT ATTAACGTTT ACAATTTCAG GTGGCACTTT	480
TCGGGGAAT GTGCGCGGAA CCCCTATTG TTTATTTTC TAAATACATT CAAATATGTA	540
TCCGCTCATG AATTAATTCT TAGAAAACT CATCGAGCAT CAAATGAAAC TGCAATTTAT	600
TCATATCAGG ATTATCAATA CCATATTTTT GAAAAAGCGG TTTCTGTAAT GAAGGAGAAA	660
ACTCACCAGG GCAGTTCCAT AGGATGGCAA GATCCTGGTA TCGGTCGCGG ATTCCGACTC	720
GTCCAACATC AATACAACCT ATTAATTTCC CCTCGTCAAA AATAAGGTTA TCAAGTGAGA	780
AATCACCATG AGTGACGACT GAATCCGGTG AGAATGGCAA AAGTTTATGC ATTTCTTTCC	840
AGACTTGTTC AACAGGCCAG CCATTACGCT CGTCATCAAA ATCACTCGCA TCAACCAAAC	900
CGTTATTCAT TCGTGATTGC GCCTGAGCGA GACGAAATAC GCGATCGCTG TAAAAAGGAC	960
AATTACAAAC AGGAATCGAA TGCAACCGGC GCAGGAACAC TGCCAGCGCA TCAACAATAT	1020
TTTCACTGA ATCAGGATAT TCTTCTAATA CCGGAATGC TGTTTTCCCG GGGATCGCAG	1080
TGGTGAGTAA CCATGCATCA TCAGGAGTAC GGATAAAATG CTTGATGGTC GGAAGAGGCA	1140
TAAATCCGT CAGCCAGTTT AGTCTGACCA TCTCATCTGT AACATCATTG GCAACGCTAC	1200
CTTTGCCATG TTTCAGAAAC AACTCTGGCG CATCGGGCTT CCCATACAAT CGATAGATTG	1260
TCGCACCTGA TTGCCGACA TTATCGCGAG CCCATTATA CCCATATAAA TCAGCATCCA	1320
TGTTGGAATT TAATCGCGGC CTAGAGCAAG ACGTTTCCCG TTGAATATGG CTCATAACAC	1380
CCCTTGATAT ACTGTTTATG TAAGCAGACA GTTTTATTGT TCATGACCAA AATCCCTTAA	1440
CGTGAGTTTT CGTCCACTG AGCGTCAGAC CCGTAGAAA AGATCAAAG ATCTTCTTGA	1500

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GATCCTTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC GCTACCAGCG	1560
GTGGTTTGTT TGCCGGGATCA AGAGCTACCA ACTCTTTTTC CGAAGGTAAC TGGCTTCAGC	1620
AGAGCGCAGA TACCAAATAC TGTCCTTCTA GTGTAGCCGT AGTTAGGCCA CCACTTCAAG	1680
AACTCTGTAG CACCGCTAC ATACCTCGCT CTGCTAATCC TGTTACCACT GGCTGCTGCC	1740
AGTGGCGATA AGTCGTGTCT TACCGGGTTG GACTCAAGAC GATAGTTACC GGATAAGGCG	1800
CAGCGGTCGG GCTGAACGGG GGGTTCGTGC ACACAGCCCA GCTTGGAGCG AACGACCTAC	1860
ACCGAACTGA GATACCTACA GCGTGAGCTA TGAGAAAGCG CCACGCTTCC CGAAGGGAGA	1920
AAGGCGGACA GGTATCCGGT AAGCGGCAGG GTCGGAACAG GAGAGCGCAC GAGGGAGCTT	1980
CCAGGGGGAA ACGCCTGGTA TCTTTATAGT CCTGTCGGGT TTCGCCACCT CTGACTTGAG	2040
CGTCGATTTT TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC CAGCAACGCG	2100
GCCTTTTAC GGTTCCTGGC CTTTGTCTGG CCTTTTGCTC ACATGTTCTT TCCTGCGTTA	2160
TCCCCTGATT CTGTGGATAA CCGTATTACC GCCTTTGAGT GAGCTGATAC CGCTCGCCGC	2220
AGCCGAACGA CCGAGCGCAG CGAGTCAGTG AGCGAGGAAG CGGAAGAGCG CCTGATGCGG	2280
TATTTTCTCC TTACGCATCT GTGCGGTATT TCACACCACA TATATGTTGC ACTCTCAGTA	2340
CAATCTGCTC TGATGCCGCA TAGTTAAGCC AGTATACACT CCGCTATCGC TACGTGACTG	2400
GGTCATGGCT GCGCCCCGAC ACCCGCCAAC ACCCGCTGAC GCGCCCTGAC GGGCTTGTCT	2460
GCTCCCGCA TCCGCTTACA GACAAGCTGT GACCGTCTCC GGGAGCTGCA TGTGTCAGAG	2520
GTTTTCACCG TCATCACCAG AACGCGCGAG GCAGCTGCGG TAAAGCTCAT CAGCGTGGTC	2580
GTGAAGCGAT TCACAGATGT CTGCCTGTTT ATCCGCGTCC AGCTCGTTGA GTTTCCTCAG	2640
AAGCGTTAAT GTCTGGCTTC TGATAAAGCG GGCCATGTTA AGGGCGGTTT TTTCTGTTT	2700
GGTCACTGAT GCCTCCGTGT AAGGGGGATT TCTGTTGATG GGGGTAATGA TACCGATGAA	2760
ACGAGAGAGG ATGCTCACGA TACGGGTAC TGATGATGAA CATGCCCGGT TACTGGAACG	2820
TTGTGAGGGT AAACAACCTGG CGGTATGGAT GCGGCGGGAC CAGAGAAAAA TCACTCAGGG	2880
TCAATGCCAG GCCTTCGTTA ATACAGATGT AGGTGTTCCA CAGGTATGCC AGCAGCATCC	2940
TGCGATGCAG ATCCGGAACA TAATGGTGCA GGGCGCTGAC TTCCGCGTTT CCAGACTTTA	3000
CGAAACACGG AAACCGAAGA CCATTTCATGT TGTGTCTCAG GTCGCAACAG TTTTGACGCA	3060
GCAGTCGCTT CACGTTCTCT CGCGTATCGG TGATTTCATC TGCTAACCCAG TAAGGCAACC	3120
CCGCCAGCCT AGCCGGGTCC TCAACGACAG GAGCACGATC ATGCGCACCC GTGGGGCCGC	3180

CATGCCGCGC	ATAATGGCCT	GCTTCTCGCC	GAAACGTTTG	GTGGCGGGAC	CAGTGACGAA	3240
GGCTTGAGCG	AGGGCGTGCA	AGATTCCGAA	TACCGCAAGC	GACAGGCCGA	TCATCGTCGC	3300
GCTCCAGCGA	AAGCGGTCT	CGCCGAAAAT	GACCCAGAGC	GCTGCCGGGA	CCTGTCCTAC	3360
GAGTTGCATG	ATAAAGAAGA	CAGTCATAAG	TGCGGCGACG	ATAGTCATGC	CCCAGGCCCA	3420
CCGGAAGGAG	CTGACTGGGT	TGAAGGCTCT	CAAGGGCATC	GGTCGAGATC	CCGGTGCCTA	3480
ATGAGTGAGC	TAACTTACAT	TAATTGCGTT	GCGCTCACTG	CCCGCTTTCC	AGTCGGGAAA	3540
CCTGTCGTGC	CAGCTGCATT	AATGAATCGG	CCAACGCGCG	GGGAGAGGCG	GTTTGCCTAT	3600
TGGGCGCCAG	GGTGGTTTTT	CTTTTCACCA	GTGAGACGGG	CAACAGCTGA	TTGCCCTTCA	3660
CCGCCTGGCC	CTGAGAGAGT	TGCAGCAAGC	GGTCCACGCT	GGTTTGCCCC	AGCAGGCGAA	3720
AATCCTGTTT	GATGTTGTTT	AACGGCGGGA	TATAACATGA	GCTGTCTTCG	GTATCGTCGT	3780
ATCCCACTAC	CGAGATATCC	GCACCAACGC	GCAGCCCGGA	CTCGGTAATG	GCGCGCAITG	3840
CGCCAGCGCG	CATCTGATCG	TTGGCAACCA	GCATCGCAGT	GGGAACGATG	CCCTCATTTCA	3900
GCATTTCAT	GTTTGTGTA	AAACCGGACA	TGGCACTCCA	GTCCGCTTCC	CGTTCGCTA	3960
TCGGCTGAAT	TTGATTGCGA	GTGAGATATT	TATGCCAGCC	AGCCAGACGC	AGACGCGCCG	4020
AGACAGAACT	TAATGGGCCC	GCTAACAGCG	CGATTTGCTG	GTGACCCAAAT	GCGACCAGAT	4080
GCTCCACGCC	CAGTCGCGTA	CGTCTTCAT	GGGAGAAAAT	AATACTGTTG	ATGGGTGTCT	4140
GGTCAGAGAC	ATCAAGAAAAT	AACGCCGGAA	CATTAGTGCA	GGCAGCTTCC	ACAGCAATGG	4200
CATCCTGGTC	ATCCAGCGGA	TAGTTAATGA	TCAGCCCACT	GACGCGTTGC	GCGAGAAGAT	4260
TGTGCACCGC	CGCTTTACAG	GCTTCGACGC	CGCTTCGTTT	TACCATCGAC	ACCACCACGC	4320
TGGCACCCAG	TTGATCGGCG	CGAGATTTAA	TCGCCGCGAC	AATTGCGAC	GGCGCGTGCA	4380
GGGCCAGACT	GGAGGTGGCA	ACGCCAATCA	GCAACGACTG	TTGCCCGGCC	AGTTGTTGTG	4440
CCACGCGGTT	GGGAATGTAA	TTCAGTCCCG	CCATCGCCGC	TTCCACTTTT	TCCCGCGTTT	4500
TCGAGAAAAC	GTGGCTGGCC	TGGTTACCA	CGCGGGAAAAC	GGTCTGATAA	GAGACACCGG	4560
CATACTCTGC	GACATCGTAT	AACGTTACTG	GTTTCACATT	CACCACCTGT	AATTGACTCT	4620
CTTCCGGGCG	CTATCATGCC	ATACCGCGAA	AGGTTTTGCG	CCATTGCGATG	GTGTCCGGGA	4680
TCTCGACGCT	CTCCCTTATG	CGACTCCTGC	ATTAGGAAGC	AGCCCAAGTAG	TAGGTTGAGG	4740
CCGTTGAGCA	CCGCCCGCCG	AAGGAATGGT	GCATGCAAGG	AGATGGCGCC	CAACAGTCCC	4800

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CCGGCCACGG	GGCCTGCCAC	CATACCCACG	CGAAACAAG	CGCTCATGAG	CCCGAAGTGG	4860
CGAGCCCGAT	CTTCCCCATC	GGTGATGTCG	GCGATATAGG	CGCCAGCAAC	CGCACCTGTG	4920
GCGCCGGTGA	TGCCGGCCAC	GATGCGTCCG	GCGTAGAGGA	TCGAGATCTC	GATCCCGCGA	4980
AATTAATACG	ACTCACTATA	GGGGAATTGT	GAGCGGATAA	CAATTCCTCC	CTAGAAATAA	5040
TTTTGTTTAA	CTTTAAGAAG	GAGATATACA	TATGGGCCAT	CATCATCATC	ATCACGTGAT	5100
CGACATCATC	GGGACCAGCC	CCACATCCTG	GGAACAGGCG	GCGGCGGAGG	CGGTCCAGCG	5160
GCGCGGGGAT	AGCGTCGATG	ACATCCGCGT	CGCTCGGGTC	ATTGAGCAGG	ACATGGCCGT	5220
GGCAGCGGCC	GGCAAGATCA	CCTACCGCAT	CAAGCTCGAA	GTGTCGTTCA	AGATGAGGCC	5280
GGCGCAACCG	AGGGGCTCGA	AACCACCGAG	CGGTTCCGCT	GAAACGGGCG	CCGGCGCCCG	5340
TACTGTCCGG	ACTACCCCGG	CGTCGTCGCC	GGTGACGTTG	GCGGAGACCG	GTAGCACGCT	5400
GCTCTACCCG	CTGTTCAACC	TGTGGGGTCC	GGCCTTTTAC	GAGAGGTATC	CGAACGTGAC	5460
GATCACCGCT	CAGGGCACCG	GTTCTGGTGC	CGGGATCGCG	CAGGCCGCCG	CCGGGACGGT	5520
CAACATTGGG	GCCTCCGACG	CCTATCTGTC	GGAAGGTGAT	ATGGCCCGCG	ACAAGGGGCT	5580
GATGAACATC	GCGCTAGCCA	TCTCCGCTCA	GCAGGTCAAC	TACAACCTGC	CCGGAGTGAG	5640
CGAGCACCTC	AAGCTGAACG	GAAAAGTCCT	GGCGGCCATG	TACCAGGGCA	CCATCAAAAC	5700
CTGGGACGAC	CGCGAGATCG	CTGCGCTCAA	CCCCGGCGTG	AACCTGCCCG	GCACCGCGGT	5760
AGTTCGCGTG	CACCGCTCCG	ACGGGTCGCG	TGACACCTTC	TTGTTCAACC	AGTACCTGTC	5820
CAAGCAAGAT	CCCGAGGGCT	GGGGCAAGTC	GCCCGGCTTC	GGCACCACCG	TCGACTTCCC	5880
GGCGGTGCGC	GGTGCCTGCG	GTGAGAACGG	CAACGGCGGC	ATGGTGACCG	GTTGCGCCGA	5940
GACACCGGGC	TGCGTGCCCT	ATATCGGCAT	CAGCTTCCTC	GACCAGGCCA	GTCACGGGG	6000
ACTCGCGGAG	GCCCCAAGTAG	GCAATAGCTC	TGGCAATTC	TTGTTGCCCG	ACGCGCAAAG	6060
CATTACGAGC	GCGGCGGCTG	GCTTCGCATC	GAAACCCCCG	GCGAACGAGG	CGATTTCGAT	6120
GATCGACGGG	CCCGCCCCGG	ACGGCTACCC	GATCATCAAC	TACGAGTACG	CCATCGTCAA	6180
CAACCGGCAA	AAGGACGCCG	CCACCGCGCA	GACCTTCGAG	GCATTTCTCG	ACTGGGCGAT	6240
CACCGACGGC	AACAAGGCCT	CGTTCCTCGA	CCAGGTTTAT	TTCCAGCCCG	TGCCGCCCGC	6300
GGTGGTGAAG	TTGTCTGACG	CGTTGATCGC	GACGATTTCC	AGCGCTGAGA	TGAAGACCGA	6360
TGCCGCTACC	CTCGCGCAGG	AGGCAGGTAA	TTTCGAGCGG	ATCTCCGGCG	ACCTGAAAAC	6420
CCAGATCGAC	CAGGTGGAGT	CGACGGCAGG	TTGTTGTCAG	GGCCAGTGGC	GCGGCGCGGC	6480

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GGGGACGGCC GCCAGGCCG CGTGGTGGC CTTCGAAGAA GCAGCCAATA AGCAGAAGCA 6540
 GGAAGCTCGAC GAGATCTCGA CGAATATTCG TCAGGCCGGC GTCCAATACT CGAGGGCCGA 6600
 CGAGGAGCAG CAGCAGGCCG TGTCTTCGCA AATGGGCTTT GTGCCCAAA CGGCCGCCCTC 6660
 GCCCGCTCG ACCGCTGCAG CGCCACCGC ACCGGCGACA CCTGTTGCC CCCACCACC 6720
 GGCCGCCGCG AACACGCCGA ATGCCAGCC GGGCGATCCC AACGCAGCAC CTCGCCCGGC 6780
 GCACCCGAAC GCACCGCCG CACCTGTCAT TGCCCCAAAC GCACCCCAAC CTGTCCGGAT 6840
 CGACAACCCG GTTGAGGAT TCAGCTTGC GCTGCCTGCT GGCTGGGTGG AGTCTGACGC 6900
 CGCCCACTTC GACTACGGTT CAGCACTCCT CAGCAAAACC ACCGGGGACC CGCCATTTC 6960
 CGGACAGCCG CCGCGCGTGG CCAATGACAC CCGTATCGTG CTCGCCCGGC TAGACCAAAA 7020
 GCTTTACGCC AGCGCCGAAG CCACCGACTC CAAGGCCGCG GCCCGGTGG GCTCGGACAT 7080
 GGGTGAGTTC TATATGCCCT ACCCGGGCAC CCGGATCAAC CAGGAAACCG TCTCGCTTGA 7140
 CGCCAAACGG GTGTCTGGAA GCGCGTCGTA TTACGAAGTC AGGTTTCAGCG ATCGAGTAA 7200
 GCCGAACGGC CAGATCTGGA CGGGCGTAAT CGGCTCGCCC GCGGCGAAGC CACCGGACGC 7260
 CGGGCCCCCT CAGCGCTGGT TTGTGGTATG GCTCGGGACC GCCAACAAAC CGGTGGACAA 7320
 GGGCGCGGCC AAGGCGCTGG CCGAATCGAT CCGGCTTTTG GTCGCCCGC CGCCGGCGCC 7380
 GGCACCGGCT CCTGCAGAGC CCGCTCCGGC GCCGGCGCGC GCGGGGAAG TCGTCTCTAC 7440
 CCCGACGACA CCGACACCGC AGCGGACCTT ACCGGCTCTA GAATTCTGCA GATATCCATC 7500
 AACTGGCGG CCGCTCGAGC ACCACCACCA CCACCACTGA GATCCGGCTG CTAACAAAGC 7560
 CCGAAAGGAA GCTGAGTTGG CTGCTGCCAC CGCTGAGCAA TAAGTAGCAT AACCCCTTGG 7620
 GGCCTCTAAA CGGGTCTTGA GGGGTTTTT GCTGAAAGGA GGAACATAT CCGGAT 7676

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met Gly His His His His His Val Ile Asp Ile Ile Gly Thr Ser
 1 5 10 15

Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg

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20	25	30
Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met		
35	40	45
Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val		
50	55	60
Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser		
65	70	75
Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro		
85	90	95
Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr		
100	105	110
Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn		
115	120	125
Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln		
130	135	140
Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser		
145	150	155
Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala		
165	170	175
Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His		
180	185	190
Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile		
195	200	205
Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn		
210	215	220
Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly		
225	230	235
Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly		
245	250	255
Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val		
260	265	270
Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys		
275	280	285
Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp		
290	295	300
Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser		
305	310	315
		320

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Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala
 325 330 335
 Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp
 340 345 350
 Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile
 355 360 365
 Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala
 370 375 380
 Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp
 385 390 395 400
 Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp
 405 410 415
 Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala
 420 425 430
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu
 435 440 445
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly
 450 455 460
 Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
 465 470 475 480
 Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser
 485 490 495
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu
 500 505 510
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala
 515 520 525
 Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro
 530 535 540
 Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro
 545 550 555 560
 Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro
 565 570 575
 Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn
 580 585 590
 Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser
 595 600 605

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Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr
 610 615 620
 Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr
 625 630 635 640
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu
 645 650 655
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu
 660 665 670
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser
 675 680 685
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys
 690 695 700
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile
 705 710 715 720
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp
 725 730 735
 Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
 740 745 750
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
 755 760 765
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala
 770 775 780
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
 785 790 795 800
 Pro Ala

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GTGGCGCGCGC	TGCGCGCGCGC	CAGCAGAGCGC	ATGTGCATCC	GTTGCGGAAC	CTGATCGCGG	60
TCGACGATGA	GCGCGCCGAA	CGCCGCGACG	ACGAAGAACG	TCAGGAAGCC	GTCACGACGC	120
GCGGTCCGCG	CGGTGACGAA	GCTGACCCCG	TCGCAGATCA	GCAGCACCCC	GCGCATGGCG	180
CCGACCAATG	TCGACCGGCT	GATCCGCGCG	ACGATCCGCA	CCACCAGCGC	CACCAGGACC	240
ACACCCAGCA	GGGCGCCGGT	GAACCGCCAG	CCGAATCCGT	TGTACCGAA	GATGGCCTCC	300

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CCGATCGCGA	TCAGCTGCTT	ACCGACCGGC	GGGTGAACCA	CCAGGCCGTA	CCCGGGGTTG	360
TCITCCACCC	CATGGTTGTT	CAGCACCTGC	CAGSCCTGGC	GGTGCCTAAT	GCTTCTCGTC	420
GAAGATGGGG	GTGCGCGCAT	CCGTCACCGA	GCCC			454

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TGCAGAAATA	CGGCGGATCC	TCGCTGGCCG	ACGCGGAACG	GATTCGCCCG	GTCCCGGAAC	60
GCATCGTCGC	CACCAAGAAG	CAAGGCAATG	ACGTCGTCGT	CGTCGCTCT	GCCATGGGGG	120
ATACCAACCGA	CGACCTGCTG	GATCTGGCTC	AGCAGGTGTG	CCCGCGCGCG	CCGCTCGGG	180
AGCTGGACAT	GCTGCTTACC	GCCGGTGAAC	GCATCTCGAA	TGCGTTGGTG	GCCATGGCCA	240
TCGAGTCGCT	CGGCGCGCAT	GCCCGGTCTG	TCACCGGTTT	GCAGGCCGGG	GTGATCACCA	300
CCGGGACCCA	CGGCAACGCC	AAGATCATCG	ACGTCAACGC	GGGCGCGGTG	CAAAACGCCC	360
TTGAGGAAGG	GCGGGTCGTC	TTGCTGGCCG	GATTCCAAGG	GGTCAGCCAG	GACACCAAGG	420
ATGTCACGAC	GTTGGGCCCG	GCGCGCTCGG	ACACCACGCG	CGTCGCCATG		470

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GGCCGGCGTA	CCCGCCCGGG	ACAAACAACG	ATCGATTGAT	ATCGATGAGA	GACGGAGGAA	60
TCGTGGCCCT	TCCCAAGTTG	ACCGACGAGC	AGCGCGCGGC	CGCGTTGGAG	AAGGCTGCTG	120
CCGCACGTCG	AGCGCGAGCA	GAGCTCAAGG	ATCGGCTCAA	GCCTGGCGGC	ACCAACCTCA	180
CCCAGGTCCT	CAAGGACGCG	GAGAGCGATG	AAGTCTTGGG	CAAAATGAAG	GTGTCGCGC	240
TGCTTGAGGC	CTTGCCAAAG	GTGGGCAAGG	TCCAGGCGC			279

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

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ACACGGTCGA	ACTCGACGAG	CCCCTCGTGG	AGGTGTCGAC	CGACAAGGTC	GACACCGAAA	60
TCCCTCGCCG	GCCGCGGGTG	TGCTGACCAA	GATCATCGCC	CAAGAAGATG	ACACGGTCGA	120
GGTCGCGCGC	GAGCTCTCTG	TCATTGGCGA	CGCCCATGAT	GCCGGCGAGG	CCGCGGTCCC	180
GGACCCCCAG	AAAGTCTCTG	CGGCGCCAAC	CCGAATCCA			219

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TCGCTGCCGA	CATCGGCGCC	GCGCCCGCCC	CCAAGCCCGC	ACCCAAGCCC	GTCCCCGAGC	60
CAGCGCCGAC	GCCGAAGGCC	GAACCCGCGC	CATCGCCGCC	GCGGCGCCAG	CCAGCCGGTG	120
CGGCCGAGGG	CGCACCGTAC	GTGACGCCGC	TGGTGCGAAA	GCTGGCGTCG	GAAAAACAAC	180
TCGACCTCGC	CGGGGTGACC	GGCACCGGAG	TGGGTGGTCG	CATCCGCAAA	CAGGATGTGC	240
TGGCCGCGGC	TGAACAAAAG	AAGCGGGCGA	AAGCACCGGC	GCCGGCGCCG	CAGGCGCCGC	300
CCGCGCCGCG	CCGAAAACGC	CGCCTGAAAG	ATCCGATGCC	GC		342

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GGGTCTTGTT	CAGTATCAGC	GCCGACGAGG	ACGCCACGGT	GCCCGTCGGC	GGCGAGTTGG	60
CCCGGATCGG	TGTCGCTGCC	GACATCGGCG	CCGCGCCCGC	CCCCAAGCCC	GCACCCAAGC	120
CCGTCCCCGA	GCCAGCGCCG	ACGCGGAAGG	CCGAACCCGC	ACCATCGCCG	CCGCGCGCCC	180
AGCCAGCCGG	TGCGGCGCAG	GGCGCACCGT	ACGTGACCGC	GCTGGTGCGA	AAGCTGGCGT	240
CGGAAAAACA	CATCGACCTC	GCGGGGGTGA	CCGGCACCGG	AGTGGGTGGT	CGCATCCGCA	300
AACAGGATGT	GCTGGCCGCG	GCTGAACAAA	AGAAGCGGGC	GAAAGCACC	GCGCCCTGAG	360
CGCTTCATCA	CCCGGTTAAC	CAGCTTGCCC	CAGAAGCCGG	CTTCGACCTC	TTGCGGGGTC	420
TTGGTCCGCT	GCAGGCGGTC	GGCGAGCCAG	TTCAGGTTAG	GCGGCGGAAA	TCTTCCAGTT	480
CGCCAGGAAG	GGCACCCCGA	ACAGGGTCCG	CACCC			515

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CCGACCCCAA	GGTGCAGATT	CAACAGGCCA	TTGAGGAAGC	ACAGCGCACC	CACCAAGCGC	60
TGACTCAACA	GGCGGCGCAA	GTGATCGGTA	ACCAGCGTCA	ATTGGAGATG	CGACTCAACC	120
GACAGCTGGC	GGACATCGAA	AAGCTTCAGG	TCAATGTGCG	CCAAGCCCTG	ACGCTGGCCG	180
ACCAGGCCAC	CGCGCCCGGA	GACGCTGCCA	AGGCCACCGA	ATACAACCAAC	GCCGCCGAGG	240
CGTTGCGAGC	CCAGCTGGTG	ACCGCCGAGC	AGAGCGTCGA	AGACCTCAAG	ACGCTGCATG	300
ACCAGGCGCT	TAGCGCCGCA	GCTCAGGCCA	AGAAGGCCGT	CGAACGAAAT	GCATGTGTGC	360
TGCAGCAGAA	GATCGCCGAG	CGAACCAAGC	TGCTCAGCCA	GCTCGAGCAG	GCGAAGATGC	420
AGGAGCAGGT	CAGCGCATCG	TTGCGGTGCA	TGAGTGAGCT	CGCCGCGCCA	GGCAACACGC	480
CGAGCCTCGA	CGAGGTGCGC	GACAAGATCG	AGCGTCGCTA	CGCCAACGCG	ATCGGTTTCG	540
CTGAACCTGC	CGAGAGT					557

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

CAGGATAGGT	TTCGACATCC	ACCTGGGTTT	CGCACCCCGT	GCGCGACCGT	GTGATAGGCC	60
AGAGGTGGAC	CTGCGCCGAC	CGACGATCGA	TGAGGAGATC	AACAGAAATG	GCCTTCTCCG	120
TCCAGATGCC	GGCACTCGGT	GAGAGCGTCA	CCGAGGGGAC	GGTTACCCGC	TGGCTCAAAC	180
AGGAAGGCGA	CACGTCGAA	CTCGACGAGC	CCCTCGTGGA	GGT		223

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAGAAGTACA	TCTGCCGGTC	GATGTCGGCG	AACCACGGCA	GCCAACCGGC	GCAGTAGCCG	60
ACCAGGACCA	CCGCATAAAG	CCAGTCCCAG	CGCACAAACA	TACGCCACCC	CGCGTATGCC	120
AGGACTGGCA	CGGCCAGCCA	CCACATCGCG	GGCGTGCCGA	CCAGCATCTC	GGCCTTGAGG	180
CACGACTGTG	CGCCGACGCC	TGCAACGTCT	TGCTGGTTCG	TGGCGTACAG	CACCGGCGCG	240
AACGACATGG	GCCAGGTCCA	CGGTTTGGAT	TCCCAAGGGT	GGTAGTTGCC	TGCGGAATTC	300
GTCAGGCCCC	CGTGGAAAGT	GAACGCTTTG	GCGGTGTATT	GCCAGAGCAT	CGGCACGGCG	360
TCGGGACAGC	GAACAACCGA	GTTGCGACCG	ACCGCTTTGAC	CGACCGCATG	CGGATCGATC	420
GCGGTCTTCG	ACGCGAACCA	CGGAGCGTAG	GTGGCCAGAT	AGACCGCGAA	CGGGATCAAC	480
CCACGCGCAT	ACCGCTGGG	AAGCAGGTCA	CGCCGCACTG	TTCCACGCCA	CGGTCTTTGC	540
ACTTGGTATG	AACGTGCGCG	CGCCACGTCA	ACGCCAGC			578

(2) INFORMATION FOR SEQ ID NO:224:

10084843.022502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

ACAACGATCG	ATTGATATCG	ATGAGAGACG	GAGGAATCGT	GGCCCTTCCC	CAGTTGACCG	60
ACGAGCAGCG	CGCGCCCGCG	TTGGAGAAGG	CTGCTGCCGC	ACGTCGAGCG	CGAGCAGAGC	120
TCAAGGATCG	GCTCAAGCGT	GGCGGCACCA	ACCTCACCCA	GGTCCTCAAG	GACGCGGAGA	180
GCGATGAAGT	CTTGGGCAAA	ATGAAGGTGT	CTGCGCTGCT	TGAGGCCCTTG	CCAAAGGTGG	240
GCAAGGTCAA	GGCGCAGGAG	ATCATGACCG	AGCTGGAAAT	TGCGCCCCAC	CCCGCCGCCT	300
TCGTGGCCTC	GGTGACCGTC	AGCGCAAGGC	CCTGCTGGAA	AAGTTCGGCT	CCGCCTAACC	360
CGACCGCCCG	ACGATGCGGG	CCGGAAGGCC	TGTGGTGGGC	GTACCCCGCG	ATACGGGGGA	420
GGAAGCGCCT	GACAGGGCCA	GCTCACAATT	CAGGCCGAAC	GCCCCGGTGG	GGGGGAACCC	480
GCCC						484

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

AGGACTGGCA	CCGCCAGCCA	CCACATCGCG	GGCGTGCCGA	CCAGCATCTC	GGCCTTGACG	60
CACGACTGTG	CGCCGACGCC	TGCAACGTCT	TGCTGGTCGA	TGGCGTACAG	CACCGGCCGC	120
AACGACTGG	GCCAGGTCCA	CGGTTTGGAT	TCCCAAGGGT	GGTAGTTGCC	TGCGGAATTC	180
GTACGCCCCG	CGTGGAAAGT	GAACGCTTTG	GCGGTGTAGT	GCCAGAGCGA	GCGCACGGCG	240
TCGGGCAGCG	GAACAACCGA	GTTGCGACCG	ACCGCTTGAC	CGACCGCATG	CCGATCGATC	300
GCGGTCTCGG	ACGCGAACCA	CGGAGCGTAG	GTGGCCAGAT	AGACCGCGAA	CGGGATCAAC	360
CCCAGCGCAT	ACCCGCTGGG	AAGCACGTCA	CGCCGCACGT	TCGCCAGCCA	CGGTCTTTGC	420
ACTTGGTACT	GACGTGCGCG	CGCCACGTGC	AACGCCAGCG	CCATCGCGCC	GAAGAACAGC	480
ACGAAGTACA	CGCCGGACCA	CTTGGTGGCG	CAAGCCAATC	CCAAGCAGCA	CCCCGGC	537

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

10084943.022502

Gly Gly Ala Ala Ala Gly Gln Gln Ser Asp Val His Pro Phe Ala Asn
 1 5 10 15
 Leu Ile Ala Val Asp Asp Glu Arg Ala Glu Arg Arg Asp Asp Glu Glu
 20 25 30
 Arg Gln Glu Ala Val Gln Gln Arg Gly Pro Arg Gly Asp Glu Ala Asp
 35 40 45
 Pro Val Ala Asp Gln Gln His Pro Gly Asp Gly Ala Asp Gln Cys Arg
 50 55 60
 Pro Ala Asp Pro Pro His Asp Pro His His Gln Arg His Gln Asp His
 65 70 75 80
 Thr Gln Gln Gly Ala Gly Glu Pro Pro Ala Glu Ser Val Val Thr Glu
 85 90 95
 Asp Gly Leu Pro Asp Arg Asp Gln Leu Leu Thr Asp Arg Arg Val Asn
 100 105 110
 His Gln Ala Val Pro Gly Val Val Phe His Pro Met Val Val Gln His
 115 120 125
 Leu Pro Gly Leu Ala Val Arg
 130 135

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Gln Lys Tyr Gly Gly Ser Ser Val Ala Asp Ala Glu Arg Ile Arg Arg
 1 5 10 15
 Val Ala Glu Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val Val
 20 25 30
 Val Val Val Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp Leu
 35 40 45
 Ala Gln Gln Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met Leu
 50 55 60
 Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile
 65 70 75 80
 Glu Ser Leu Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala Gly
 85 90 95
 Val Ile Thr Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr
 100 105 110
 Pro Gly Arg Leu Gln Thr Ala Leu Glu Glu Gly Arg Val Val Leu Val
 115 120 125
 Ala Gly Phe Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu
 130 135 140
 Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Met
 145 150 155

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Pro Ala Tyr Pro Ala Gly Thr Asn Asn Asp Arg Leu Ile Ser Met Arg
 1             5             10             15
Asp Gly Gly Ile Val Ala Leu Pro Gln Leu Thr Asp Glu Gln Arg Ala
 20             25             30
Ala Ala Leu Glu Lys Ala Ala Ala Arg Arg Ala Arg Ala Glu Leu
 35             40             45
Lys Asp Arg Leu Lys Arg Gly Gly Thr Asn Leu Thr Gln Val Leu Lys
 50             55             60
Asp Ala Glu Ser Asp Glu Val Leu Gly Lys Met Lys Val Ser Ala Leu
 65             70             75             80
Leu Glu Ala Leu Pro Lys Val Gly Lys Val Gln Ala
 85             90

```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Thr Val Glu Leu Asp Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val
 1             5             10             15
Asp Thr Glu Ile Pro Ser Pro Ala Ala Gly Val Leu Thr Lys Ile Ile
 20             25             30
Ala Gln Glu Asp Asp Thr Val Glu Val Gly Gly Glu Leu Ser Val Ile
 35             40             45
Gly Asp Ala His Asp Ala Gly Glu Ala Ala Val Pro Ala Pro Gln Lys
 50             55             60
Val Ser Ala Gly Pro Thr Arg Ile
 65             70

```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

Ala Ala Asp Ile Gly Ala Ala Pro Ala Pro Lys Pro Ala Pro Lys Pro
 1           5           10           15
Val Pro Glu Pro Ala Pro Thr Pro Lys Ala Glu Pro Ala Pro Ser Pro
      20           25           30
Pro Ala Ala Gln Pro Ala Gly Ala Ala Glu Gly Ala Pro Tyr Val Thr
      35           40           45
Pro Leu Val Arg Lys Leu Ala Ser Glu Asn Asn Ile Asp Leu Ala Gly
 50           55           60
Val Thr Gly Thr Gly Val Gly Gly Arg Ile Arg Lys Gln Asp Val Leu
 65           70           75
Ala Ala Ala Glu Gln Lys Lys Arg Ala Lys Ala Pro Ala Pro Ala Ala
      85           90           95
Gln Ala Ala Ala Ala Pro Ala Pro Lys Ala Pro Pro Glu Asp Pro Met
      100          105          110
Pro

```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

Val Leu Val Ser Ile Ser Ala Asp Glu Asp Ala Thr Val Pro Val Gly
 1           5           10           15
Gly Glu Leu Ala Arg Ile Gly Val Ala Ala Asp Ile Gly Ala Ala Pro
      20           25           30
Ala Pro Lys Pro Ala Pro Lys Pro Val Pro Glu Pro Ala Pro Thr Pro
      35           40           45
Lys Ala Glu Pro Ala Pro Ser Pro Pro Ala Ala Gln Pro Ala Gly Ala
 50           55           60
Ala Glu Gly Ala Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Ser
 65           70           75           80
Glu Asn Asn Ile Asp Leu Ala Gly Val Thr Gly Thr Gly Val Gly Gly
      85           90           95
Arg Ile Arg Lys Gln Asp Val Leu Ala Ala Glu Gln Lys Lys Arg
      100          105          110
Ala Lys Ala Pro Ala Pro
      115

```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

Asp Pro Lys Val Gln Ile Gln Gln Ala Ile Glu Glu Ala Gln Arg Thr
 1           5           10           15
His Gln Ala Leu Thr Gln Gln Ala Ala Gln Val Ile Gly Asn Gln Arg
 20           25           30
Gln Leu Glu Met Arg Leu Asn Arg Gln Leu Ala Asp Ile Glu Lys Leu
 35           40           45
Gln Val Asn Val Arg Gln Ala Leu Thr Leu Ala Asp Gln Ala Thr Ala
 50           55           60
Ala Gly Asp Ala Ala Lys Ala Thr Glu Tyr Asn Asn Ala Ala Glu Ala
 65           70           75           80
Phe Ala Ala Gln Leu Val Thr Ala Glu Gln Ser Val Glu Asp Leu Lys
 85           90           95
Thr Leu His Asp Gln Ala Leu Ser Ala Ala Ala Gln Ala Lys Lys Ala
100          105          110
Val Glu Arg Asn Ala Met Val Leu Gln Gln Lys Ile Ala Glu Arg Thr
115          120          125
Lys Leu Leu Ser Gln Leu Glu Gln Ala Lys Met Gln Glu Gln Val Ser
130          135          140
Ala Ser Leu Arg Ser Met Ser Glu Leu Ala Ala Pro Gly Asn Thr Pro
145          150          155          160
Ser Leu Asp Glu Val Arg Asp Lys Ile Glu Arg Arg Tyr Ala Asn Ala
165          170          175
Ile Gly Ser Ala Glu Leu Ala Glu Ser
180          185

```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

Val Ser Thr Ser Thr Trp Val Pro His Pro Val Arg Asp Arg Val Ile
 1           5           10           15
Gly Gln Arg Trp Thr Cys Ala Asp Arg Arg Ser Ile Glu Glu Ser Thr
 20           25           30
Glu Met Ala Phe Ser Val Gln Met Pro Ala Leu Gly Glu Ser Val Thr
 35           40           45
Glu Gly Thr Val Thr Arg Trp Leu Lys Gln Glu Gly Asp Thr Val Glu
 50           55           60
Leu Asp Glu Pro Leu Val Glu
 65           70

```

(2) INFORMATION FOR SEQ ID NO:234:

7084843.022507

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

Glu Val His Leu Pro Val Asp Val Gly Glu Pro Arg Gln Pro Thr Gly
 1           5           10           15
Ala Val Ala Asp Gln Asp His Arg Ile Thr Pro Val Pro Ala His Lys
          20           25           30
His Thr Pro Pro Arg Val Cys Gln Asp Trp His Arg Gln Pro Pro His
          35           40           45
Arg Gly Arg Ala Asp Gln His Leu Gly Leu Asp Ala Arg Leu Cys Ala
          50           55           60
Ala Ala Cys Asn Val Leu Leu Val Asp Gly Val Gln His Arg Pro Gln
          65           70           75           80
Arg His Gly Pro Gly Pro Arg Phe Gly Phe Pro Arg Val Val Val Ala
          85           90           95
Cys Gly Ile Arg Gln Ala Arg Val Glu Val Glu Arg Phe Gly Gly Val
          100          105          110
Leu Pro Glu Arg Ala His Gly Val Gly Gln Arg Asn Asn Arg Val Ala
          115          120          125
Thr Asp Arg Leu Thr Asp Arg Met Pro Ile Asp Arg Gly Leu Gly Arg
          130          135          140
Glu Pro Arg Ser Val Gly Gly Gln Ile Asp Arg Glu Arg Asp Gln Pro
          145          150          155          160
Gln Arg Ile Pro Ala Gly Lys His Val Thr Pro His Cys Ser Gln Pro
          165          170          175
Arg Ser Leu His Leu Val
          180

```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

Asn Asp Arg Leu Ile Ser Met Arg Asp Gly Gly Ile Val Ala Leu Pro
 1           5           10           15
Gln Leu Thr Asp Glu Gln Arg Ala Ala Leu Glu Lys Ala Ala Ala
          20           25           30
Ala Arg Arg Ala Arg Ala Glu Leu Lys Asp Arg Leu Lys Arg Gly Gly
          35           40           45
Thr Asn Leu Thr Gln Val Leu Lys Asp Ala Glu Ser Asp Glu Val Leu
          50           55           60

```

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Gly Lys Met Lys Val Ser Ala Leu Leu Glu Ala Leu Pro Lys Val Gly
 65 70 75 80
 Lys Val Lys Ala Gln Glu Ile Met Thr Glu Leu Glu Ile Ala Pro His
 85 90 95
 Pro Ala Ala Phe Val Ala Ser Val Thr Val Ser Ala Arg Pro Cys Trp
 100 105 110
 Lys Ser Ser Ala Pro Pro Asn Pro Ala Gly Arg Arg Cys Gly Pro Glu
 115 120 125
 Gly Leu Trp Trp Ala Tyr Pro Arg Ile Arg Gly Arg Ser Gly Leu Thr
 130 135 140
 Gly Pro Ala His Asn Ser Gly Arg Thr Pro Arg Trp Gly Gly Thr Arg
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Asp Trp His Arg Gln Pro Pro His Arg Gly Arg Ala Asp Gln His Leu
 1 5 10 15
 Gly Leu Asp Ala Arg Leu Cys Ala Ala Ala Cys Asn Val Leu Leu Val
 20 25 30
 Asp Gly Val Gln His Arg Pro Gln Arg His Gly Pro Gly Pro Arg Phe
 35 40 45
 Gly Phe Pro Arg Val Val Val Ala Cys Gly Ile Arg Gln Ala Arg Val
 50 55 60
 Glu Val Glu Arg Phe Gly Gly Val Val Pro Glu Arg Ala His Gly Val
 65 70 75 80
 Gly Gln Arg Asn Asn Arg Val Ala Thr Asp Arg Leu Thr Asp Arg Met
 85 90 95
 Pro Ile Asp Arg Gly Leu Gly Arg Glu Pro Arg Ser Val Gly Gly Gln
 100 105 110
 Ile Asp Arg Glu Arg Asp Gln Pro Gln Arg Ile Pro Ala Gly Lys His
 115 120 125
 Val Thr Pro His Cys Pro Gln Pro Arg Ser Leu His Leu Val Leu Thr
 130 135 140
 Ser Arg Arg His Val Glu Arg Gln Arg His Arg Ala Glu Glu Gln His
 145 150 155 160
 Glu Val His Ala Gly Pro Leu Gly Gly Ala Ser Gln Ser Gln Ala Ala
 165 170 175
 Pro Arg

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
 (B) TYPE: nucleic acid

10084843.022502

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

ATGCCAAGCC	GGTCTGATG	CCCGAGCTCG	GCGAATCGGT	GACCGAGGGG	ACCGTCATTC	60
GTTGGCTGAA	GAAGATCGGG	GATTCGGTTC	AGGTTGACGA	GCCACTCGTG	GAGGTGTCCA	120
CCGACAAGGT	GGACACCGAG	ATCCCGTCCC	CGGTGGCTGG	GGTCTTGGTC	AGTATCAGCG	180
CCGACGAGGA	CGCCACGGTG	CCCGTCGGCG	GCGAGTTGGC	CCGGATCGGT	GTGCTGCGCG	240
AGATCGGCGC	CGCGCCCGCC	CCCAAGCCCC	C			271

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Ala	Lys	Pro	Val	Leu	Met	Pro	Glu	Leu	Gly	Glu	Ser	Val	Thr	Glu	Gly
1				5				10						15	
Thr	Val	Ile	Arg	Trp	Leu	Lys	Lys	Ile	Gly	Asp	Ser	Val	Gln	Val	Asp
			20					25					30		
Glu	Pro	Leu	Val	Glu	Val	Ser	Thr	Asp	Lys	Val	Asp	Thr	Glu	Ile	Pro
			35				40						45		
Ser	Pro	Val	Ala	Gly	Val	Leu	Val	Ser	Ile	Ser	Ala	Asp	Glu	Asp	Ala
			50				55					60			
Thr	Val	Pro	Val	Gly	Gly	Glu	Leu	Ala	Arg	Ile	Gly	Val	Ala	Ala	Glu
			65			70				75				80	
Ile	Gly	Ala	Ala	Pro	Ala	Pro	Lys	Pro							
							85								

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GAGGTAGCGG	ATGSCCGGAG	GAGCACCCCA	GGACCGCGCC	CGAACCGCGG	GTGCGCGTCA	60
TCGATATGTG	GGCACCGTTC	GTTCCGTCCG	CCGAGGTCAT	TGACGAT		107

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

ATGAAGTTGA	AGTTTGCTCG	CCTGAGTACT	GC	GATACTGG	GT	TGTGCAGC	GGCGCTTGTG	60
TTTCCTGCCT	CGGTTGCCAG	CGCAGATCCA	CCT	GACCCGCG	AT	CAGCCGGA	CATGACGAAA	120
GGCTATTGCC	CGGGTGGCCG	ATGGGGTTTT	GG	C	CGTGTGCGA	CGGCGAGAAG		180
TACCCCGACG	GCTCGTTTTG	GCACCACTGG	AT	GCAAACGT	GGTTTACCGG	CCCACAGTTT		240
TACTTCGATT	GTGTCAGCGG	CGGTGAGCCC	CT	CCCCGGCC	CGCCGCCACC	GGGTGGTTGC		300
GGTGGGGCAA	TTCGTCCTCA	GCAGCCCAAC	G	TCCCTGA				339

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met	Lys	Leu	Lys	Phe	Ala	Arg	Leu	Ser	Thr	Ala	Ile	Leu	Gly	Cys	Ala
1			5						10					15	
Ala	Ala	Leu	Val	Phe	Pro	Ala	Ser	Val	Ala	Ser	Ala	Asp	Pro	Pro	Asp
			20					25					30		
Pro	His	Gln	Pro	Asp	Met	Thr	Lys	Gly	Tyr	Cys	Pro	Gly	Gly	Arg	Trp
		35					40					45			
Gly	Phe	Gly	Asp	Leu	Ala	Val	Cys	Asp	Gly	Glu	Lys	Tyr	Pro	Asp	Gly
		50				55					60				
Ser	Phe	Trp	His	Gln	Trp	Met	Gln	Thr	Trp	Phe	Thr	Gly	Pro	Gln	Phe
		65				70				75				80	
Tyr	Phe	Asp	Cys	Val	Ser	Gly	Gly	Glu	Pro	Leu	Pro	Gly	Pro	Pro	Pro
			85						90				95		
Pro	Gly	Gly	Cys	Gly	Gly	Ala	Ile	Pro	Ser	Glu	Gln	Pro	Asn	Ala	Pro
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

10084843.022502

GTGACCACGG TGGGCCTGCC ACCAACCCTG GCAGCGGCAG CCGCGCGGC GCCGCGGCT 60
 CCGGCGGCAA CGGTGGCGCC GGGGGTAACG CCACCGGCTC AGGCGGCAAG GCGGCGCGC 120
 GTGGCAATGG CGGTGATGGG AGCTTCGGCG CTACCAAGCG CCCCGCTCC ATCGGGGTCA 180
 CGGGCGCCCC CGGCGGCAAC GCGGCAAGG GCGGCGCGG TGGCAGCAAC CCAACGGCT 240
 CAGGTGGCGA CCGCGGCAAA GCGGCAACG GCGGTGCCG GCGCAACGG GGCTCGATCG 300
 GCGCCAACAG CGGCATCGTC GCGGTTCCT GTGGGGCCG TGGCGCTGGC GCGCGCGCG 360
 GAAACGGCAG C 371

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GTCCGGGTCC CACCACCGCG CCGGCGCGCC CCTAGCGGCC GGGCGCACCA GCCCTTTTC 60
 TTGACTCGTT CAAGAAAAGG GCCTTCTGTT TGGTCGSCCA TGTTGGCATG ATCGTGACCC 120
 ATGGGCAACA TCAGCGTCGA CATCTCGGCC AAGGTCTAGC TCCATGCGAA TCGCCGCGCG 180
 GGTGGTGAGC ATCGGTCTAG CCGTCATAGC AGGGTTCGCG GTACCTGTTG CCGACGCACA 240
 CCCGTCGGAG CCGGGGGTTG TGTCTACGC GGTGCTCGGA AAGGGGTCGG TCGGCAACAT 300
 CGTCGGCGCC CCAATGGGGT GGGAGGCGGT GTTCACCAAG CCGTTCAGG CGTTTGGGT 360
 CGAACTACCG GCGTGCAACA ACTGGGTGGA CATCGGCTG CCCGAGGTG ACGACGATCC 420
 CGAC 424

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

GCGATGGCGG CCGCGGTAC CACGCCAAT GTGGAACGGT TTCCTAACCC CAACGATCCT 60
 TTGCATCTGG CGTCAATTGA CTTACGCCG GCCGATTTCG TCACCGAGGG CCACCGTCTA 120
 AGGGCGGATG CGATCTTACT GCGCCGTACC GACCGGCTGC CTTTCGCGGA GCGCGCGGAT 180
 TGGGACTTGG TGGAGTCGCA GTTGCGCACG ACCGTACCG CCGACACGGT GCGCATCGAC 240
 GTCATCGCGC ACGATATCGC TCCGAACTG GCGGCGGCGT CCAAACTCAC CGAATCGCTG 300
 CGGCTCTAGC ATTCTGTC 317

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

1008483.022502

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

TGGCGTATGC	GCTTCGCAGC	CGGTGCCGCG	TCAACGCGCC	GGAGGCAATC	GCTTCGCTGC	60
CGAGGAATGG	TTCGATCAGC	ATCGCAGTGT	GCCGTCGTGC	ACCGACACCG	CCGTCCAACG	120
TGAATCGAGG	GCGGAAAATC	GGCCGAAATC	TCGCCCTCAG	TTACGCTCG	GCGCCTAACG	180
GTTCTGGAAG	ITGGGTGCGC	GCTTCTCGGC	GAACGCGCGC	GGGCCTTCCT	TGGCGTCGTC	240
GGACAGGAAG	ACCTTGTATG	CGATCTGGGT	GTCGATCTTG	AACGCCCTCGT	TTTCGGGCAT	300
GCACTCGGTC	TCGCGGATGG	ACCGCAAGAT	GGCCTGCACG	GCCAGGGGTC	CGTTAGCCGA	360
GATGGCGTCG	GCAAGTTCTA	GAACCTTGGT	CAACGCGCTGG	CCGTCGGGCA	CACGTGGCCG	420
AT						422

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GCGTGCCGCT	GAACACCAGC	CCGCGGCTGC	CAGATCTCCC	GGACTCGGTA	GTGCCGCCGG	60
TGGCGTCGTT	GCTCTCTGTA	CGGGGCGCGG	CGACCATAAG	GTGCTAATG	CCCAGGTAGC	120
GGCCAGGTG	CATGGAGTCG	ATGATGATGC	GACTCTCCAG	CTGCCGAC	GGGAGCTTGG	180
CATCGGGCCT	GATCAGCCAG	GACGCGTAGG	ACAAGTCGAT	CGAATGCATA	GTGGCCTCCA	240
GAGTGGCCGT	GCCACTTCCG	GCGTGCTCCA	CGGCAAATGC	CTTGATTCTT	AGCTCCGCGT	300
AGTGTTCGCG	CATCGCCTGC	GGGATGAATG	GGAACCCGAG	GATGGCGACA	AACGGGTCGT	360
ACCTCAGGTT	TGCCGCTTTG	CGCACAGTGG	TCGACAGCCG	GTACTCGGCA	TAAATGCTGG	420
CCCCGA						426

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

AGACCGGCGA	GGGTGTGGTC	GCTGCCGCGC	GCATTGTCGA	TAATCTGCGC	TGGGTGACG	60
CGCCGATCAA	CTAGTGAGGC	GCAACGCTAG	GCCTTGGGAT	ACCCACAGCT	AAAAAGTTTA	120
TCAAAGAAAC	GAAGAAGGTT	GCCATGAGCA	CTGTTGCCGC	CTACGCCGCC	ATGTGCGCGA	180
CCGAACCCCT	GACCAAGACC	ACGATCACCC	GTCGCGACCC	GGGCGCGCAC	GACATGGCGA	240
TCGACATCAA	ATTGCGCGGA	ATCTGTGCGT	CGGACATCCA	TACCGTCCAA	ACCGAATGGG	300
GGCAACCGAA	TTTACCTGTG	GTCCCTG				327

10084843.022502

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Asp His Gly Gly Pro Ala Thr Asn Pro Gly Ser Gly Ser Arg Gly Gly
 1 5 10 15
 Ala Gly Gly Ser Gly Gly Asn Gly Gly Ala Gly Gly Asn Ala Thr Gly
 20 25 30
 Ser Gly Gly Lys Gly Gly Ala Gly Gly Asn Gly Gly Asp Gly Ser Phe
 35 40 45
 Gly Ala Thr Ser Gly Pro Ala Ser Ile Gly Val Thr Gly Ala Pro Gly
 50 55 60
 Gly Asn Gly Gly Lys Gly Gly Ala Gly Gly Ser Asn Pro Asn Gly Ser
 65 70 75 80
 Gly Gly Asp Gly Gly Lys Gly Gly Asn Gly Gly Ala Gly Gly Asn Gly
 85 90 95
 Gly Ser Ile Gly Ala Asn Ser Gly Ile Val Gly Gly Ser Gly Gly Ala
 100 105 110
 Gly Gly Ala Gly Gly Ala Gly Gly Asn Gly Ser
 115 120

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Met Ala Ala Ala Gly Thr Thr Ala Asn Val Glu Arg Phe Pro Asn Pro
 1 5 10 15
 Asn Asp Pro Leu His Leu Ala Ser Ile Asp Phe Ser Pro Ala Asp Phe
 20 25 30
 Val Thr Glu Gly His Arg Leu Arg Ala Asp Ala Ile Leu Leu Arg Arg
 35 40 45
 Thr Asp Arg Leu Pro Phe Ala Glu Pro Pro Asp Trp Asp Leu Val Glu
 50 55 60
 Ser Gln Leu Arg Thr Thr Val Thr Ala Asp Thr Val Arg Ile Asp Val
 65 70 75 80
 Ile Ala Asp Asp Met Arg Pro Glu Leu Ala Ala Ser Lys Leu Thr
 85 90 95
 Glu Ser Leu Arg Leu Tyr Asp Ser
 100

205220.24648007

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```

Ala Tyr Ala Leu Arg Ser Arg Cys Arg Val Asn Ala Pro Glu Ala Ile
 1             5             10             15
Ala Ser Leu Pro Arg Asn Gly Ser Ile Thr Ile Ala Val Cys Arg Arg
                20             25             30
Ala Pro Thr Pro Pro Ser Asn Val Asn
 35             40

```

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

```

Val Pro Leu Asn Thr Ser Pro Arg Leu Pro Asp Leu Pro Asp Ser Val
 1             5             10             15
Val Pro Pro Val Ala Ser Leu Leu Ser
                20             25

```

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

```

Met Ser Thr Val Ala Ala Tyr Ala Ala Met Ser Ala Thr Glu Pro Leu
 1             5             10             15
Thr Lys Thr Thr Ile Thr Arg Arg Asp Pro Gly Pro His Asp Met Ala
                20             25             30
Ile Asp Ile Lys Phe Ala Gly Ile Cys Arg Ser Asp Ile His Thr Val
 35             40             45

```

205220.24878001

Gln Thr Glu Trp Gly Gln Pro Asn Leu Pro Val Val Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GCTTGGAGCC	CTGGAGCGAC	GGTGTGGGTC	TGGGGGTGCGA	TTCGTTCTCG	GCGAAAGTCA	60
ACTAAAGACC	ACGTTGACAC	CCAACCGGCG	GCCCGGCATG	GGCGTCGCG	GCGTAGAAGC	120
TTTGACCGCG	GCGCGAAAGC	TTGCTGCTG	CGGCCCATGC	AGATCGCACA	CGCTTGCTTG	180
AACATCGGGT	GGAGCCGGTG	GTACGCCAG	GCT			213

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CCGAGCTGCT	GTTCCGGCGCC	GGCGGTGCGG	GCGGCGCGGG	TGGGGCGGGC	ACCGACGGCG	60
GGCCCGGTGC	TACCGGCGGG	ACCGGCGGAC	ACGGCGGAGT	CGGCGCGCAC	GGCGGATGGC	120
TGGCACCCGG	CGGGGCCGGC	GGGGCCGGCG	GGCAAGGCGG	GGCAGGTGGT	GCCCGCAGCG	180
ATGGTGGCGC	GTTGGGTGGT	ACCGGCGGGA	CGGGCGGTAC	CGGCGGCGCC	GGTGGCGCCG	240
GCGGTGCGGG	CACACTGCTG	CTGGGCGCTG	GCGGACAGGG	CGGCCTCGCG	GGCGCCGCGC	300
GACAAGGCGG	CACCGGCGGG	GGCGGCGGGA	GATGCGGTTC	TGGGGGGTGT	CAGTGGCACT	360
GGTGGTA						367

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

AAGGCGTGAT	TGGCAAGGCG	ACCGCGCAGC	GGCCCGTAGC	CGCGGGACGG	CCCAAGCCCC	60
GACCGCAGCG	GCCGGTGCTC	GACCGGGTCA	GCGACCAGCG	GCGCTGACCG	TGCCGCTCGT	120
CTACTTCGAC	GCCAGCGCCT	TGCTCAAAC	TCTACCACC	GAGACAGGGA	GCTCGCTGGC	180

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GTCCGCTCTA TGGGACGGCT GCGACGCCGC ATTGTCCAAC CGCCTGGCCT ACCCCGAAGT 240
 CCGCGCCGCA CTCGCTGCAA CGGGCCGCAA TCACGACCTA ACCGAATCCG AGCTCGCCGA 300
 CGCCGAGCGT GACTGGGAGG ACTTCTGGGC CGCACCCGCC CAGTCGAACCT CACCGCGACG 360
 GTTGAACAGC ACGCCGGGCA CCTCGCCCGA ACACATGCCT TACGGGGAGC CGACACCGTT 420

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

CTCTTGTCGG TGGCATCGCG GGTACCGCGC GAACCGCGCG CAACGCCGGT ATGCTCGCCG 60
 GCGCGCCGCG GCGCGCGCGT GCGCGCGCGT TCAGCTTCAG CACTGCCGGT GGGGCTGGCG 120
 GCGCGCGCGG GCGCGGTGGG CTGTTACCA CCGCGCGTGT CGCGCGCGCC GGTGGGCGAG 180
 GTACACGCGG CGGGGCGGGC GCGCGCGCGG GGGCGCGCGG GTTGTTTGGT GCCGGCGGCA 240
 TGGGCGGGGC GGGCGGATTC GGGGATCACG GAACGCTCGG CACCGCGCGG GCGGCGCGG 299

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Leu Glu Pro Trp Ser Asp Gly Val Gly Leu Gly Val Asp Ser Phe Ser
 1 5 10 15
 Ala Lys Val Asn
 20

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Glu Leu Leu Phe Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly
 1 5 10 15
 Thr Asp Gly Gly Pro Gly Ala Thr Gly Gly Thr Gly Gly His Gly Gly

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(2) INFORMATION FOR SEQ ID NO:259:

(A) LENGTH: 34 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

(2) INFORMATION FOR SEQ ID NO:260:

(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Leu	Val	Gly	Gly	Ile	Gly	Gly	Thr	Gly	Gly	Thr	Gly	Gly	Asn	Ala	Gly
1				5					10					15	
Met	Leu	Ala	Gly	Ala	Ala	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Phe	Ser	Phe
		20						25					30		
Ser	Thr	Ala	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Leu	Phe
		35					40					45			
Thr	Thr	Gly	Gly	Val	Gly	Gly	Ala	Gly	Gly	Gln	Gly	His	Thr	Gly	Gly
	50					55					60				
Ala	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Leu	Phe	Gly	Ala	Gly	Gly	Met
65					70					75				80	

Gly Gly Ala Gly Gly Phe Gly Asp His Gly Thr Leu Gly Thr Gly Gly
 85 90 95
 Ala Gly Gly

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

TCCTGTTCCG	CGCCGGCGGG	GTGGGCGGTG	TGGGCGGTGA	CGGTGTGGCA	TTCTGGGGCA	60
CCGCCCCCGG	CGGGCCCGGT	GGTGCCGGCG	GGGCCGGTGG	GCTGTTTCAGC	GTCCGTGGGG	120
CCGGCGGGCG	CGCGCGGAATC	GGATTGTGTCG	GGAACAGCGG	TGCCGGGGGG	TCCGGCGGGT	180
CCGCCCTGCT	CTGGGGCGAC	GGCGGTGCCG	GC GGCGCGGG	TGGGGTTCGG	TCCACTACCG	240
CGGTGCCGG	CGGGCGGGG	GGCAACGCCA	GCCTGCTGGT	AA		282

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

CGGCACGAGC	CGTGCTACTG	GTCAACTGAT	GCCCTGATTG	TGACCTTCCC	GGCGCCGGAT	60
CAGTGCTTCT	CAGGACCGAC	GTAATATTTC	AAAACCAATC	CGGCCGCCGA	GGCGAGGATG	120
AATGCCACAC	CGCGGGCGAT	CAGCCACGGG	AGCCACAACG	CGATGCCGAC	CGCTGCCACC	180
GAGCCGACAC	ACGCGACCAT	GATCGGCCAC	CAGCTATGCG	GA CTGAAGAA	TCCAAGTTCT	240
CCTGCGCGGT	CGCTGATTTC	AGCGCCTTCG	TAGTCCTCGG	GCCGGGAATC	TAACCGGCGG	300
GCCACAAACC	GGAAGAAGGT	GGCGACGATC	AACGCCATGC	CGCCGGTGAG	CGCCAACGCA	360
ATGSTGCCAC	CCCACTCGAC	ACCACCGGTG	GCGAACATCG	AGGTCAACAC	GCCGT	415

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TCACCGCGTG	AACGGTTCGT	AACACTGATA	CGTATGCTTG	TCACGAGCA	GATCAAGTCC	60
AGTCCGACCA	ATGCCAGGAG	ATCATCGGCT	AGGCTCAAGG	TTCGCGCTGG	GACGAGACGG	120
TATTGAGTTC	TGGCGTTGGA	CGGTCCGTGG	CGTGGTGGGA	AGTCTGACGC	GGCATCAGAA	180
CGGTTGTCAA	TACCACTCTT	TGGGGGATAT	GGCCTATTGG	GTGCTGTCGG	GCGCTCCAC	240
CGGATCCGTT	TTCGAACGTT	GCGCAAGCGC	GGTCCAGTTA	CGGCCTGTTC	ACTGCGCGCT	300
GGCGTAGCTG	CGCGCCCTCG	ATCGGTTTGA	ACGTCATCGC	AATTCGCCCA	ATGGGTGAGT	360
ACCTGACGCT	CCT					373

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

CCAAACCGGA	CAGGCCGGCA	GCGACGGTCG	GAAGTTGCAC	CACGGTGCGC	GCTCCATGTA	60
GCCAAACCGT	GACCACGGCG	TAGACAGCAG	ATCCGTGGAT	CGCGCGTTCG	GTGTCGTCCG	120
GGCCGAGTAC	CGCGGGGCGG	AACCGCAGCG	ACCAAAGCAA	CGCGATCGAT	ACGGGGATCG	180
CCACTCGTGC	CGAATTTCAG	CTCCGTCGAC	AAGCTTGCAG	CCGCACTCGA	ACCCGGGTGA	240
ATGATTGAGT	TTAAACCGCT	TAGCAATAAC	TAGCATAACC	CCTTGGGGCC	TCTAAACGGG	300
TCTTGAGGGG	TTTTTTGCTG	AAAGGAGGAA	CTATATCCGG	ATACCTGGC	GTAGTAGCGA	360
AGAGGCCCGC	ACCGATCGCC	CTTCCCAACA	GTTGCGCAGC	CTGAATGGCG	AATGGACGCG	420
CCC						423

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

AGTGGCCAGC	CGGTCCGCCA	ATGCATCCAG	CTCCCGGTAC	GTCAGCTGAC	CATCCGCCCA	60
ACTGACCGCC	CCAGAGTCAG	GCTGTGCCGC	AGCGATTTCG	GCGAACCGGG	TATGACCCGC	120
GGGTGCCGAG	GTGTCACAT	CCGGCAGGCC	GGGTGCGGTC	GGATCGTGCT	CGCGTCCAG	180
CAGAATGTGC	ACGTCCGCCA	GCGGCCGATC	CCACCGGCTG	ACCAAGCGCT	GTAACACAGC	240
CAGCACCCGC	CTGCCGAGGC	TTTCGGGCGC	CATCGTGCCC	AGCGCACCGT	CGAGCACCTC	300
CAGTAGCAGC	GTGAGCTCAC	CGGTGCTGCG	GTGCGCGCGC	ACGGCTCACCG	GAAGAGTGCGA	360
CAAACCTCTT	AGCGCCACCG	GACGGAAGCT	CACCCGTTT	GCGA		404

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GTCTCTGGTCG	CAGGCTGTTC	TTCGAACCCG	CTGGCTAACT	TCGCACCCGG	GTATCCGCC	60
ACCATCGAAC	CGGCCAAC	GGCGGTGTCA	CGCCTACTT	CGCAAGACCC	GGCCGGTGCA	120
GTGCGACCAC	TGAGCGGCCA	CCCCCGGGCG	GCATATTTCG	ACAACGGCAC	CCGCCAATTG	180
GTGGCTCTGC	GCCCGGGCGC	CGATTTCGGC	GCACCCGCCA	GCATCATGGT	CTTCGATGAC	240
ATGCACGTTG	CACCGCGCGT	CATTTTCTG	CCGGGCCCGG	CAGCCGCGTT	GACCAGCGAC	300
GACCACGGCA	CGGCCTTCT	TGCCGCCCGC	GGCGGCTACT	TCGTGGCCGA	CCTGTCCTCC	360
GGTCACACCG	CACGAGTAA	TGTCGCTGAC	GCAGCGCACA	CCGATTTCAC	CGCGATCGCC	420
C						421

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

ATGCATATCA	CGCTCAACGC	CATCTCGCGT	GCGATCTTCG	GGGCGGGCGG	CAGTGAACCTA	60
GACGAGCTGC	GCCGCTCAT	TCCGCCGTGG	GTACGCTGG	GCTCGCGCTT	GGCGCGCTA	120
CCGAAACCCA	AACGCGACTA	TGGCCGCTT	AGCCCGTGGG	GCCGGCTGGC	CGAGTGGCGG	180
CGCCAGTACG	ACACTGTAT	CGACGAGCTC	ATCGAAGCCG	AGCGGGCCGA	CCGCAACTTC	240
GCCGATCCGA	CCGAGCTTTT	GGCGTTGATG	CTGCGCAGCA	CTTACGACGA	CGGTTCCATC	300
ATGTCCGCGA	AGGACATTGG	CGACGAACTG	CTCAGCTGTC	TTGCCCGCGG	GCACGAAACC	360
ACGGCGGCGA	CATGGGCTGG	GCGTTCGAAC	GGCTCAACCG	GCACCCGCGC	GTGCTCGCGG	420
CTCTGG						426

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GTCTCTGGTCG	CAGGCTGTTC	TTCGAACCCG	CTGGCTAACT	TCGCACCCGG	GTATCCGCC	60
ACCATCGAAC	CGGCCAAC	GGCGGTGTCA	CGCCTACTT	CGCAAGACCC	GGCCGGTGCA	120
GTGCGACCAC	TGAGCGGCCA	CCCCCGGGCG	GCATATTTCG	ACAACGGCAC	CCGCCAATTG	180
GTGGCTCTGC	GCCCGGGCGC	CGATTTCGGC	GCACCCGCCA	GCATCATGGT	CTTCGATGAC	240
GTGCACGTTG	CACCGCGCGT	CATTTTCTG	CCGGGCCCGG	CAGCCGCGTT	GACCAGCGAC	300
GACCACGGCA	CGGCCTTCT	TGCCGCCCGC	GGCGGCTACT	TCGTGGCCGA	CCTGTCCTCC	360
GGTCACACCG	CACGAGTAA	TGTCGCTGAC	GCAGCGCACA	CCGATTTCAC	CGCGATCGCC	420

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CGCCGCTCCG ACGGCAAGCT GGTGCTGGGC AGCGCAGATG GCGCCGTCTA CACGCTTGCC 480
 AAGAACC CGC AGTTGACCG CGTCGGCGCC GCCACCGTAG CC 522

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GCTGGGGCGC	ACCGCCGTCC	GGCGGGCCCA	GCCCTTGGGC	CCAGACCCCG	CGCAAAACCA	60
ACCCGTGGCC	CTTAGTGGCC	GGCGCCGCGC	CCGTCTGTCT	CGTCTCTGTG	TTGGGCGCCA	120
TCGGCATCTG	GATCGCCATC	CGGCCCAAGC	CGGTACAGCC	GCCTCAGCCG	GTTCGCGAGG	180
AGCGCCTTAG	CGCCTTACTG	CTGAATCTCT	CAGAAGTCAA	CGCCGTGATG	GGCTCGTCGT	240
CCATGCGAGC	GGGCAAACCG	ATCACATCGA	TGGACTCTTC	GCCGGTGACG	GTGTCCCTGC	300
CGGACTGCCA	GGGCGCGCTG	TATACGAGCC	AGGATCCGGT	GTATGCCGGC	ACCGGCTACA	360
CGGCCATCAA	CGGCTTGATT	TCATCCGAGC	CGGGCGACAA	CTACGAACAT	TGGGTGAACC	420
AAGCCGTCTG	CGCCTTTCCG	ACCGCCGACA	AAGCCCGCGC	GTTCGTGACG	ACTTCGGCCG	480
ACAAATGGAA	GAATCGCGCA	GGCAAGACGG	TCACCGTCAC	GAATAAGGCC	AAGACCTACC	540
GGTGGAGCTT	TGCCGAGCTC	AAAGGCAGCC	CGCCGACGAT	CACGGTGATA	GACACCCAAG	600
AAGGCGCTGA	GGGCTGGGAA	TGCCAACGCG	CGATGAGCGT	GGCCAACAAT	GTGGTTGTCT	660
ACGTCAACGC	ATGCGGGTAC	CAGATCACCA	ATCAAGCAGG	CCAGATCGCC	GCCAAGATCT	720
GTTGACAAAG	TCAACAAG					739

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

AGAGCTCGTC	GAGGCGGCCA	TCGCCCGCGC	CGAAGCCGTT	AACCCGGCAC	TGAACGCGTT	60
GGCGTATGC						69

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

202520.24848007

ACTGCACCCG	GCAGGCGCGA	CCAAACGGATC	GGGTCAACTA	GCACTGCCGG	TGGAGGCGCC	60
CCCGCGGTCT	GTGCTTCC	ACGGGGAACC	CTTGGGCAGC	GCGGCTCCAG	AAGGGTTGGA	120
GGGAGAGTTC	GACGACCGTA	TCGACGAGCG	GTTCCCGGTC	TTCAGCTCGG	CCAGTCTCGC	180
CGAAGCGCTG	CCGGGTCCGC	TGACCCCGAT	GACGCTGGAT	GTCCAGTTGA	GTGGACTGCG	240
CGCGGCCGGT	CGGGCGATGG	GTGCGGTACT	GGCGCTTGGC	GGTGTCTGTT	CCGATGAGTG	300
GGAGAGAAGA	GCCATCGCGG	TGTTGCGTCA	CCGCCCGTAT	ATCGAGTGT	CGGCAATAT	360
TGTGGCCGCC	GCCCAACTGC	CGGGGTGGGA	CGCGCAGGCC	GTAACCCGGC	GGGCACTGGG	420
CGAGCAACCG	CAGGTCACTG	AGCTGCTTCC	GTTTGGTCGA	CCGCAACTTG	CGGGCGGACC	480
GCTCGGCTCG	GTGCGCAAGG	TGGTCGTGAC	GGCACGGTCG	CTG		523

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GTGTCGGTGT	CGTCGGGGTA	GGAGCGACTT	CCCCGGCCGG	CGCCGGCGCC	GGAGCGGGCT	60
CTGCAGGAAC	CGGTGCCGGC	GCCGGCGGCG	GGGCGACCAA	AGGCCGGATC	GATTCGGCCA	120
CGCCTTTGGC	CGCGCCCTTG	TCCACCGGGT	TGTTGGCGGT	CCCCGAGCAT	ACCACAAACC	180
AACGCTGAGG	GGGCCCGGCG	TCCGGTTCGT	TCGCCCGGCG	CGAC		224

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TGAAGTGACT	GCCCCGCTCG	ATCGGCGGCG	GCGGCGGTGC	ATAGCTGCGC	CGCCAGGCCA	60
TGAAGTGCTC	TTCCGCATAG	CGGGCCTTGG	TCTCGGCCTT	GTCCAAACCC	TGCAGCGCGC	120
CGTAGTGGCG	TTGCTTGAGC	CGCCAGCTAC	GCCGACGCGG	AATCCAGAGC	CGATCGGCGC	180
TGTCCAAGCG	CAGATGCGCG	GTGGTGATCG	CGCGCCGCGC	CAACGAGGTG	TAGAGCAGCT	240
CGGGCAATAG	GTCTGTCTCC	GCGATCAGCT	CGCGGCTTTC	AACCGCCTCT	GCCTGGCCCT	300
TGTCGCTCAG	GCCGACATCG	ACCCAGCCCG	TGAACAGGTT	GAGGGCATTC	CAGTCGCTCT	360
CGCCGTCGCG	CAGCAACACC	AGGCTGCCAG	TGTTTGCCAT	ACCGCAAGT	CTCTCACGCA	420
CTCCGCACT	CCTCATCGTG	GACCAAAATG	CCCGAATTC	CCTCGGTCCG	CTCGCAGCG	480
CGTTCATACC	GCCGAGGTGG	TCGGCACCGT	AACGGCCGGT	T		521

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CTCCAGGCTC	ATTCGCTCGA	ACAAAGCCAC	CCGGCCGTAC	AGCGGACGCC	CCCATTCGTT	60
GTCTGATAG	TCGCGGTACA	GCTGGGCATC	GGGCCCTGGA	CGAACCTCCG	CCCAGGGGCA	120
GCGAACACAG	CCGTGCGCGC	TCACGCGGGG	TCAGAACGGT	AGTGACAGAC	AGTCTCGCCG	180
CGCGAAGGTT	TTGACGCGTC	AGACTCGGCC	TCGGCGTCTT	CCGACGAGGC	GTGGATCGCC	240
CCGAGCTGAG	AGCGTAGCGC	CTCGAGCTCA	CGGCCGAGCC	GTTCAGCAC	CCAGTCCACC	300
TCGCTGGTCT	TGTTCCCGCG	CAGCACCTGC	GTGAACCTGA	CCGCGTCGAC	ATCGGCGCGG	360
GTGACCCCGA	ACGCGGCGAG	CGTCTCGCC	GTCCTCGCCC	GCGGACGGGG	CGCAACTGC	420
TCGCCA						426

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GCGGACACGG	CGGACAAAGC	GCAATCGGCC	TCGGCGGCGG	CGCCGCGCGC	GACGGGGGCC	60
AGGGCGGCGC	CGGCCCGCGA	CTGTGGGGTA	CTGGCGGCGC	CGGCGGACAC	GGCGGGGCAA	120
GGCGGTGGTA	CCGGGGGGCC	ACCGCTGCC	GGTCAGGCAG	GCATGGGCGC	CGCGGGTGGC	180
GCGGTGGGCG	TGATCGGCAA	CGGCGGGGCC	GGCGGCGGAC			219

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

AAGATCATCG	GCGCCGCTCC	TTAGCATCGC	TGGCTCTGCG	ATCGTCGCGG	GCGCGGATCA	60
CGGAGGTCCG	GCCTTGTACC	CCACTCCTCG	AACGGTCAGC	ACCACAGTCG	GGTTCCTCGG	120
ATCCTTTTTC	ACCTTGGGCC	GCAGACGCTG	GACATGCACG	TTCAACAGCC	TGGTATCGCG	180
TGGGTGCCGG	TAACCCCATTA	CCTGTTGAG	CAGCACATCA	CGAGTAAACA	CCTGGCGCGG	240
CTTGCGCGCG	AATGCGACCA	ACAGGTCGAA	TTCCAGCGGT	GTCAACGAGA	TCTGCTCACC	300
GTTGCGAGTG	ACCTTGTGCG	CCGGTACGTC	GATTCTTACG	TCGGCGATGG	ACAGCATCTC	360
GGCGGGTTCG	TCGTGGTTGC	GGCGCAGCGC	CGCCCGCACC	CGCGCAACCA	GCTCTGTTGG	420
CTTGAACGCG	TTCATGATGT	AGTCGTCGGC	GCCCGACTCC	AGACCCAGCA	CCACATCCAC	480
GGTGTGCGTC	TTTGCGGTGA	GCATCAGCAT	CGGAACACCG	GAATCGGCGC	GCAACACCCG	540
GCACACGTCG	ATCGCGTTCA	TACCGGGGCA	A			571

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```

Leu Phe Gly Ala Gly Gly Val Gly Gly Val Gly Gly Asp Gly Val Ala
 1           5           10           15
Phe Leu Gly Thr Ala Pro Gly Gly Pro Gly Gly Ala Gly Gly Ala Gly
      20           25           30
Gly Leu Phe Ser Val Gly Gly Ala Gly Gly Ala Gly Gly Ile Gly Leu
 35           40           45
Val Gly Asn Ser Gly Ala Gly Gly Ser Gly Gly Ser Ala Leu Leu Trp
 50           55           60
Gly Asp Gly Gly Ala Gly Gly Ala Gly Gly Val Gly Ser Thr Thr Gly
 65           70           75           80
Gly Ala Gly Gly Ala Gly Gly Asn Ala Ser Leu Leu Val
      85           90

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Met Pro Pro Val Ser Ala Asn Ala Met Val Pro Ala His Ser Thr Pro
 1           5           10           15
Pro Val Ala Asn Ile Glu Val Asn Thr Pro
      20           25

```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

10084843.022502

Lys Pro Asp Arg Pro Ala Ala Thr Val Gly Ser Cys Thr Thr Val Arg
 1 5 10 15
 Ala Pro Cys Ser Gln Pro Val Thr Thr Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Trp Pro Ala Gly Arg Pro Met His Pro Ala Pro Gly Thr Ser Ala Asp
 1 5 10 15
 His Pro Pro Asn
 20

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1 5 10 15
 Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
 20 25 30
 Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
 35 40 45
 Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
 50 55 60
 Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
 65 70 75 80
 Met His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
 85 90 95
 Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
 100 105 110
 Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
 115 120 125
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala
 130 135 140

(2) INFORMATION FOR SEQ ID NO:282:

10084943.022502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

Met His Ile Thr Leu Asn Ala Ile Leu Arg Ala Ile Phe Gly Ala Gly
 1           5           10           15
Gly Ser Glu Leu Asp Glu Leu Arg Arg Leu Ile Pro Pro Trp Val Thr
          20           25           30
Leu Gly Ser Arg Leu Ala Ala Leu Pro Lys Pro Lys Arg Asp Tyr Gly
          35           40           45
Arg Leu Ser Pro Trp Gly Arg Leu Ala Glu Trp Arg Arg Gln Tyr Asp
          50           55           60
Thr Val Ile Asp Glu Leu Ile Glu Ala Glu Arg Ala Asp Pro Asn Phe
65           70           75           80
Ala Asp Arg Thr Asp Val Leu Ala Leu Met Leu Arg Ser Thr Tyr Asp
          85           90           95
Asp Gly Ser Ile Met Ser Arg Lys Asp Ile Gly Asp Glu Leu Leu Thr
          100          105          110
Leu Leu Ala Ala Gly His Glu Thr Thr Ala Ala Thr Trp Ala Gly Arg
          115          120          125
Ser Asn Gly Ser Thr Gly Thr Pro Thr Cys Ser Arg Leu Trp
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1           5           10           15
Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
          20           25           30
Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
          35           40           45
Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
          50           55           60
Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
65           70           75           80
Val His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
          85           90           95
Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
          100          105          110

```

J008484.022502

Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
 115 120 125
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala Arg Arg Ser Asp
 130 135 140
 Gly Lys Leu Val Leu Gly Ser Ala Asp Gly Ala Val Tyr Thr Leu Ala
 145 150 155 160
 Lys Asn Pro

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Trp Gly Ala Pro Pro Ser Gly Gly Pro Ser Pro Trp Ala Gln Thr Pro
 1 5 10 15
 Arg Lys Thr Asn Pro Trp Pro Leu Val Ala Gly Ala Ala Val Val
 20 25 30
 Leu Val Leu Val Leu Gly Ala Ile Gly Ile Trp Ile Ala Ile Arg Pro
 35 40 45
 Lys Pro Val Gln Pro Pro Gln Pro Val Ala Glu Glu Arg Leu Ser Ala
 50 55 60
 Leu Leu Leu Asn Ser Ser Glu Val Asn Ala Val Met Gly Ser Ser Ser
 65 70 75 80
 Met Gln Pro Gly Lys Pro Ile Thr Ser Met Asp Ser Ser Pro Val Thr
 85 90 95
 Val Ser Leu Pro Asp Cys Gln Gly Ala Leu Tyr Thr Ser Gln Asp Pro
 100 105 110
 Val Tyr Ala Gly Thr Gly Tyr Thr Ala Ile Asn Gly Leu Ile Ser Ser
 115 120 125
 Glu Pro Gly Asp Asn Tyr Glu His Trp Val Asn Gln Ala Val Val Ala
 130 135 140
 Phe Pro Thr Ala Asp Lys Ala Arg Ala Phe Val Gln Thr Ser Ala Asp
 145 150 155 160
 Lys Trp Lys Asn Cys Ala Gly Lys Thr Val Thr Val Thr Asn Lys Ala
 165 170 175
 Lys Thr Tyr Arg Trp Thr Phe Ala Asp Val Lys Gly Ser Pro Pro Thr
 180 185 190
 Ile Thr Val Ile Asp Thr Gln Glu Gly Ala Glu Gly Trp Glu Cys Gln
 195 200 205
 Arg Ala Met Ser Val Ala Asn Asn Val Val Val Asp Val Asn Ala Cys
 210 215 220
 Gly Tyr Gln Ile Thr Asn Gln Ala Gly Gln Ile Ala Ala Lys Ile Cys
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

10084843.022502

- (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

Asp Val Val Glu Ala Ala Ile Ala Arg Ala Glu Ala Val Asn Pro Ala
 1           5           10           15
Leu Asn Ala Leu Ala Tyr
                20
  
```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Leu His Pro Ala Gly Ala Thr Asn Gly Ser Gly Gln Leu Ala Leu Pro
 1           5           10           15
Val Glu Ala Pro Pro Arg Ser Val Pro Ser His Gly Glu Pro Leu Gly
                20           25           30
Ser Ala Ala Pro Glu Gly Leu Glu Gly Glu Phe Asp Asp Arg Ile Asp
                35           40           45
Glu Arg Phe Pro Val Phe Ser Ser Ala Ser Leu Ala Glu Ala Leu Pro
 50           55           60
Gly Pro Leu Thr Pro Met Thr Leu Asp Val Gln Leu Ser Gly Leu Arg
 65           70           75           80
Ala Ala Gly Arg Ala Met Gly Arg Val Leu Ala Leu Gly Gly Val Val
                85           90           95
Ala Asp Glu Trp Glu Arg Arg Ala Ile Ala Val Phe Gly His Arg Pro
                100           105           110
Tyr Ile Gly Val Ser Ala Asn Ile Val Ala Ala Gln Leu Pro Gly
                115           120           125
Trp Asp Ala Gln Ala Val Thr Arg Arg Ala Leu Gly Glu Gln Pro Gln
                130           135           140
Val Thr Glu Leu Leu Pro Phe Gly Arg Pro Gln Leu Ala Gly Gly Pro
 145           150           155           160
Leu Gly Ser Val Ala Lys Val Val Val Thr Ala Arg Ser Leu
                165           170
  
```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

Val Gly Val Val Gly Val Gly Ala Thr Ser Pro Ala Gly Ala Gly Ala
 1          5          10          15
Gly Ala Gly Ser Ala Gly Thr Gly Ala Gly Ala Gly Gly Gly Ala Thr
 20          25          30
Lys Gly Arg Ile Asp Ser Ala Ser Ala Leu Ala Ala Pro Leu Ser Thr
 35          40          45
Gly Leu Leu Ala Val Pro Ser His Thr Thr Asn Gln Arg
 50          55          60

```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```

Met Ala Asn Thr Gly Ser Leu Val Leu Leu Arg His Gly Glu Ser Asp
 1          5          10          15
Trp Asn Ala Leu Asn Leu Phe Thr Gly Trp Val Asp Val Gly Leu Thr
 20          25          30
Asp Lys Gly Gln Ala Glu Ala Val Arg Ser Gly Glu Leu Ile Ala Glu
 35          40          45
His Asp Leu Leu Pro Asp Val Leu Tyr Thr Ser Leu Leu Arg Arg Ala
 50          55          60
Ile Thr Thr Ala His Leu Ala Leu Asp Ser Ala Asp Arg Leu Trp Ile
 65          70          75          80
Pro Val Arg Arg Ser Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu
 85          90          95
Gln Gly Leu Asp Lys Ala Glu Thr Lys Ala Arg Tyr Gly Glu Glu Gln
100          105          110
Phe Met Ala Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Ile Glu
115          120          125
Arg Gly Ser Gln Phe
130

```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

2025032408001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

Pro Gly Ser Phe Ala Arg Thr Lys Pro Pro Gly Arg Thr Ala Asp Ala
 1           5           10           15
Pro Ile Arg Cys Arg Asp Ser Arg Gly Thr Ala Gly His Arg Ala Leu
 20           25           30
Asp Glu Pro Pro Arg Gly Ser Glu Pro Ala Arg Arg Ser Arg
 35           40           45
Gly Val Arg Thr Val Val His Asp Ser Leu Ala Ala Arg Arg Val
 50           55           60

```

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

Gly His Gly Gly Gln Ser Ala Ile Gly Leu Gly Gly Gly Ala Gly Gly
 1           5           10           15
Asp Gly Gly Gln Gly Gly Ala Gly Arg Gly Leu Trp Gly Thr Gly Gly
 20           25           30
Ala Gly Gly His Gly Gly Ala Arg Arg Trp Tyr Arg Gly Pro Thr Ala
 35           40           45
Ala Arg Ser Gly Arg His Gly Arg Arg Gly Trp Arg Arg Trp Ala Asp
 50           55           60
Arg Gln Arg Arg Gly Arg Arg Arg
 65           70

```

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

```

Asp His Arg Arg Ser Leu Ala Ser Leu Arg Ser Ala Ser Ser Pro
 1           5           10           15
Ala Arg Ile Thr Glu Val Arg Pro Cys Thr Pro Leu Leu Glu Arg Ser
 20           25           30
Ala Pro Gln Ser Gly Ser Arg Asp Pro Phe Arg Pro Trp Pro Ala Asp
 35           40           45
Ala Gly His Ala Arg Ser Pro Ala Trp Tyr Arg Leu Gly Ala Gly Asn
 50           55           60

```

202503240004

Pro Ile Pro Val Arg Ala Ala His His Glu
65 70

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

CCGCACGTAA	CACCGTGAAT	TGAAGGGAGC	CGCTGGTTCAT	GGGCCGATTG	TATCCGTGGG	60
CGAACGGTTA	TTGACGGCCC	GGAGGCCACT	CCGCTGCCAC	CAAGTGGTGA	CTCAGCGCGT	120
TTTCACGGCA	ACGAACGGCG	GACACACCAC	TTGACATTGC	ACAGCACGGC	CGCG	174

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

TCGCAACACGG	GGTGACGTTG	CGTCCGGTGG	CGCTAGAGAG	TTTGTGCGAC	TTTCCGGTGA	60
CCGTGCGCCG	GCACCGCAGC	ACCGGTGAGC	TCACGCTGCT	AGTGGAGGTG	CTCGACGGTG	120
CGCTGGGCAC	GATGGCGCCC	GAAAGCCTCG	GCAGGCGGGT	GCTGGCTGTG	TTACAGCGCT	180
TGGTCAGCCG	GTGGGATCGG	CCGCTGCGCG	ACGCTCGACAT	TCTGCTGGAC	GGCGAGCACG	240
ATCCGACCGC	ACCCGGCCTG	CCGGATGTGA	CGACGTCGGC	ACCCGCGGTG	CATACCCGGT	300
TCGCCGAAAT	CGCTGCGGCA	CAGCCTGACT	CGGTGGCGGT	CAGTTGGGCG	GATGGTGCAG	360
TGACGTACCG	GGAGCTGGAT	GCATTGGCCG	ACCGGCTGGC	CACT		404

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Ala	Asn	Gly	Val	Thr	Phe	Arg	Pro	Val	Ala	Leu	Glu	Ser	Leu	Ser	His
1				5					10				15		
Phe	Pro	Val	Thr	Val	Ala	Ala	His	Arg	Ser	Thr	Gly	Glu	Leu	Thr	Leu
	20							25					30		

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Leu Val Glu Val Leu Asp Gly Ala Leu Gly Thr Met Ala Pro Glu Ser
 35 40 45
 Leu Gly Arg Arg Val Leu Ala Val Leu Gln Arg Leu Val Ser Arg Trp
 50 55 60
 Asp Arg Pro Leu Arg Asp Val Asp Ile Leu Leu Asp Gly Glu His Asp
 65 70 75 80
 Pro Thr Ala Pro Gly Leu Pro Asp Val Thr Thr Ser Ala Pro Ala Val
 85 90 95
 His Thr Arg Phe Ala Glu Ile Ala Ala Ala Gln Pro Asp Ser Val Ala
 100 105 110
 Val Ser Trp Ala Asp Gly Gln Leu Thr Tyr Arg Glu Leu Asp Ala Leu
 115 120 125
 Ala Asp Arg Leu Ala Thr
 130

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GCTTCGACGG	CTACGAGTAC	CTGTTCTGGG	TGGGTGTGTC	GGGCGCCTAC	GACGACAAGG	60
CCAAGAAGAC	CACCAAGGCC	GTCCGCCGAG	TGTTTCGCCGT	CGCCGGGGTG	AAATACTTGG	120
TGCTGGGGCG	TGGGGAAACC	TGCAACGGCG	ACTCGCGCGC	CCGCTCCGGC	AACGAGTTCC	180
TCTTCCAGCA	GCTGGCAACA	CAGGCCGTCG	AGACCCTGGA	CGGTTTGTTT	GAGGGTGTGG	240
AGACCGTCGA	CCGCAAGATC	GTTGTCACT	GCCCGCACTG	CTTCAACACC	ATCGGCAAGG	300
AATATCGGCA	GCTGGGGGCC	AACTACACCG	TGCTGCACCA	CACCCAGCTG	CTCAATCGGT	360
TGCTGCGCGA	CAAGAGGCTG	GTCCCTGTCA	CTCCGGTTTC	TCAGGACATC	ACCTACCACG	420
ACCCGTGCTA	CCTGGGTCCG	CACAACAAGG	TCTACGAGGC	ACCACGGGAG	CTGATCGGTG	480
CCGCGGGGGC	CACCTGAGCC	GAGATGCCCG	GCCATGCCGA	CCGCAG		526

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

CTCGCCGCGG	TGATCTGGCC	GGCGAACTTC	GTCAGTGCAT	CCAGACCCCA	ACGATCATCG	60
ATCAGGCCGA	TGCCCATGAT	CACCGCACCG	GCCACCAGCA	CCGCGGGCAT	GCCGGTGGAA	120
TAGAGGAACC	CCCGGGTAGG	TGCCGGAAGC	TGGGAGGCCA	GAAAGACGGC	GCCGACATAG	180
CCCAGGAACA	TGCCCAACCC	ACCCATCCGA	GGGGTAGGCG	TGACGTGCAC	ATCTCGCTCC	240
CGCGGGTAGG	CGACGGCTCC	CAGGCGACTG	GCCAGCATCC	GCACCGGACC	GGTCGCAAAA	300
TAGGTGATGA	TGCGCGGGT	CAGCCGAGC	AGCGCAAGCT	CACGACGCGG	GACACCGGCG	360

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CCGCGATAGG ACAGGGCGAG CAAGCCACCG GCAACGCCGG CCACATCGCT GGACACCTCG 420
 AGACCGTACT GCACCAACCT GAAGAGCTGA AACTCGCCG AACGTGCAAC AGCTGCGAAC 480
 AATTGGG 487

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

ACGAAGCGCG AGAATATGAG CCGGGGCAAC CCGGCATGTA CGAGCTTGAG TTCCCGGCGC 60
 CTCAGCTGTC GTCGTCCGAC GGCCGTGGTC CGGTGTGGT GCACGCTTG GAAGGTTTCT 120
 CCGACGCCCG CCATGCGATC CGGCTGGCCG CCGCCCACT CAAGGCGGCC CTGGACACAG 180
 AGCTGGTCGC GTCCTTCGCG ATCGATGAAC TACTGGAATA CCGCTCGCGG CGGCCATTAA 240
 TGACTTTCAA GACCGATCAT TTCACCACT CCGATGATCC TGAGCTAAGC CTGTATGCGC 300
 TGC CGCAGAC CATCGGCACC CCATTTCTGC TGCTGGCGGG TTTGGAGCCG GACCTGAAGT 360
 GGGAGCGGTT CATCACGCC GTCCGATTGC TGGCCGAGCG CCTGGGTGTA CGGCAGAACC 420
 ATCGCGCTGG GCACCGTCCC GATGGCGGTT CCGCACACAC GACCGATCAC GATGACCGCT 480
 CATTCCAACA ACCGGGAGCT ATCTCGATT TTCAACCGTT CGATCTCC 528

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

CCAAGCCCGT CAAGGAGCCG GTGCCGGCCT TGCCTCCGGT GCCGCCGACG CCGGCGTTGC 60
 CGCCGTTGCC GCCGTTGCCG CCGGTACCGG GGTTCCTTAC GGTGCCCGCG CCGGCAGCA 120
 TGGCCCGGCT GTTTAGGCCG TTTTCGCCGG CCCC CGCGTC ACCGCTTTG CCGCCATCGC 180
 CGCCGTTGCC GCCGCTGGTG GGGGTGGCGG CCTGGTTGAC GTATTGTTC ACCGGCCCGG 240
 CCCTTGACCC TTTGGCGGTG TCGATCGCGG CGTCGATGGA TCCGCCGACC ACGACGTGCG 300
 AAGCCTCGCC TGCCGCCGCA GCCGCCAAC TGTGTCGCGG CTCCTGCGAT TTGGCCCGCG 360
 CCGACGAGAT GATGGGCACC ACCGAGGCT GCGGCCGTCT GGGGAGGCC AGCGCGGGTT 420
 CGCGGTACG CCATACGCGA CGGTGCGCCG CCGCTTCGGA GATTGTGAG CTGCGTTGCA 480
 CCAGATCGAG CACGGGTGTG CCGAGGACT GGGTTAGCCC GTTGGCGCCG CCGTTGTAGC 540
 GGGGAGCGCA ATATCGGTGC CCACTGACC CAACCGCGAC TCATAAGCG ACACATTTCG 600
 CGGTTGATGC 610

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid

10084843-022502

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

Phe Asp Gly Tyr Glu Tyr Leu Phe Trp Val Gly Cys Ala Gly Ala Tyr
 1          5          10          15
Asp Asp Lys Ala Lys Lys Thr Thr Lys Ala Val Ala Glu Leu Phe Ala
 20          25          30
Val Ala Gly Val Lys Tyr Leu Val Leu Gly Ala Gly Glu Thr Cys Asn
 35          40          45
Gly Asp Ser Ala Arg Arg Ser Gly Asn Glu Phe Leu Phe Gln Gln Leu
 50          55          60
Ala Gln Gln Ala Val Glu Thr Leu Asp Gly Leu Phe Glu Gly Val Glu
 65          70          75
Thr Val Asp Arg Lys Ile Val Val Thr Cys Pro His Cys Phe Asn Thr
 85          90          95
Ile Gly Lys Glu Tyr Arg Gln Leu Gly Ala Asn Tyr Thr Val Leu His
100          105          110
His Thr Gln Leu Leu Asn Arg Leu Val Arg Asp Lys Arg Leu Val Pro
115          120          125
Val Thr Pro Val Ser Gln Asp Ile Thr Tyr His Asp Pro Cys Tyr Leu
130          135          140
Gly Arg His Asn Lys Val Tyr Glu Ala Pro Arg Glu Leu Ile Gly Ala
145          150          155          160
Ala Gly Ala Thr

```

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

```

Arg Arg Arg Asp Leu Ala Gly Glu Leu Arg Gln Cys Ile Gln Thr Pro
 1          5          10          15
Thr Ile Ile Asp Gln Ala Asp Ala His Asp His Arg Thr Gly His Gln
 20          25          30
His Arg Gly His Ala Gly Gly Ile Asp Glu Pro Pro Gly Glu Cys Arg
 35          40          45
Lys Leu Gly Gly Lys Lys Asp Gly Ala Asp Asn Ala Gln Glu His Arg
 50          55          60
Gln Pro Thr His Pro Arg Gly Arg Arg Asp Val His Ile Ser Leu Pro
 65          70          75          80
Arg Val Gly Asp Gly Ser Gln Ala Thr Gly Gln His Pro His Arg Thr
 85          90          95
Gly Arg Lys Ile Gly Asp Asp Arg Arg Gly Gln Pro Asp Gln Arg Lys

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10084843.022502

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          100          105          110
Leu Thr Gln Arg Asp Thr Gly Ala Ala Ile Gly Gln Gly Glu Gln Ala
      115          120          125
Thr Gly Asn Ala Gly His Ile Ala Gly His Leu Glu Thr Val Leu His
      130          135          140
Gln Pro Glu Glu Leu Asn Thr Arg Arg Thr Cys Asn Ser Cys Glu Gln
      145          150          155          160
Leu

```

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

```

Glu Ala Arg Glu Tyr Glu Pro Gly Gln Pro Gly Met Tyr Glu Leu Glu
 1          5          10          15
Phe Pro Ala Pro Gln Leu Ser Ser Ser Asp Gly Arg Gly Pro Val Leu
      20          25          30
Val His Ala Leu Glu Gly Phe Ser Asp Ala Gly His Ala Ile Arg Leu
      35          40          45
Ala Ala Ala His Leu Lys Ala Ala Leu Asp Thr Glu Leu Val Ala Ser
      50          55          60
Phe Ala Ile Asp Glu Leu Leu Asp Tyr Arg Ser Arg Arg Pro Leu Met
      65          70          75          80
Thr Phe Lys Thr Asp His Phe Thr His Ser Asp Asp Pro Glu Leu Ser
      85          90          95
Leu Tyr Ala Leu Arg Asp Ser Ile Gly Thr Pro Phe Leu Leu Leu Ala
      100          105          110
Gly Leu Glu Pro Asp Leu Lys Trp Glu Arg Phe Ile Thr Ala Val Arg
      115          120          125
Leu Leu Ala Glu Arg Leu Gly Val Arg Gln Asn His Arg Pro Gly His
      130          135          140
Arg Pro Asp Gly Arg Ser Ala His Thr Thr Asp His Asp Asp Arg Ser
      145          150          155          160
Phe Gln Gln Pro Gly Ala Ile Ser Asp Phe Gln Pro Phe Asp Leu
      165          170          175

```

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

1008497.022507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Lys Pro Val Lys Glu Pro Val Pro Ala Leu Pro Pro Val Pro Pro Thr
 1 5 10 15
 Pro Ala Leu Pro Pro Leu Pro Pro Leu Pro Pro Val Pro Gly Phe Pro
 20 25 30
 Thr Val Pro Pro Gly Ser Met Ala Pro Leu Phe Arg Pro Phe Ser
 35 40 45
 Pro Ala Pro Pro Ser Pro Ala Leu Pro Pro Ser Pro Pro Leu Pro Pro
 50 55 60
 Leu Val Gly Val Ala Ala Trp Leu Thr Tyr Cys Ser Thr Gly Pro Ala
 65 70 75 80
 Leu Asp Pro Leu Ala Val Ser Ile Ala Ala Ser Met Asp Pro Pro Thr
 85 90 95
 Thr Thr Cys Glu Ala Ser Pro Ala Ala Ala Ala Gln Leu Cys Arg
 100 105 110
 Gly Ser Cys Asp Leu Ala Pro Ala Asp Glu Met Met Gly Thr Thr Gly
 115 120 125
 Ala Cys Gly Arg Leu Gly Glu Ala Ser Ala Gly Ser Arg Ser Arg His
 130 135 140
 Thr Arg Arg Cys Ala Ala Ala Ser Glu Ile Cys Arg Leu Arg Cys Thr
 145 150 155 160
 Arg Ser Ser Ser Gly Val Pro Arg Asp Trp Val Ser Pro Leu Ala Pro
 165 170 175
 Pro Leu

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

AATTCGGCAC GARCAGCACC AACACCGGCT TCTTCAACTC CGGCGACGTC AATACCGGTA 60
 TCGGCACACAC CGGCAGCTTC AACACCGGCA GCTTCAATCC GGGCGATTCC AACACCGGGG 120
 ATTTCAACCC ANGCACTAC CACACGGGGA CTCGGAACA CCGGCGATT TACACCGGCS 180
 CCTTCATCTC CGGCAGCTAC AGCAACGGGT CTGTGGAGT GGAAATTATC AGGGCTCATT 240
 GGNTGCACCC GGSCTTRCGA ATCCCTCGKG CCAATTCAAC TCCTCNACAA GCTTGC GGCC 300
 GCACTCSAGC CGGGGTGAAT GATTGAGTTT AACCGCTNAN CAATAACTAG CATAACCCCT 360
 TKGCGCCTCT AAACGGGTCT TGAAGGGTTT TTTGCTGAAA GGANGAATA TATCCGGATA 420
 ACTGGCGGTAN TACGAAAAGC CGCACCGATC GCCTTCCCAA CAGTTGCGCA CCKGAATGGC 480
 AATGGACCNC CCTKTTACCG GSCATTAACTN CGGGGGTGTN GKGOTTACCC CCACGTNACC 540
 GCTACCTTGC CANNSSCTN RSGCGTCTT TCSITTTCTC CTTCCTTCTC CCMCTTCGCC 600
 GGTTCCCTTC AGCTCTAAAT CGGGGNNCCC TTTMGGGTTC CAATTATTGC TTACNGSCCC 660
 CCACCCCAA AAYTNATNG GGTTAATGTC CCTTMTTGGG NTCCCCCTA WTNANNGT 720
 TCCCCCTTNA CTTTGRSTCC CTTCYTATW NTGAMNCTNT TTCCACYGGA AAAMNCTCCA 780
 CCNTYSSGS TTTCTTTGA WTTATMRGR AATTSCAATY CCGCYTTKGG TTMAANTTAA 840
 CYTATTTTCA ATTTTCCCGM TTTTMMNATR TTNSNCKCGM KNCTCCNRKA SSGNTTTCCT 900
 CCCCCVTSS GKTYCCCRN G 921

10084843.022502

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

AATTCGGCAC GAGATANGGG CGCACCAGGG TCCGCAGCCG GCGGGACCGT CGCCAGCACC 60
 ACCGGGGTCA ACAGCACCAC GGTGGCGTCC ANGCAAGCGC CGCGGTGAT GCGGCGCGAG 120
 ACGGCRAACA CCTGCCGTAG CAGTCGGTGC GACTCCGCGC TCGCTCGANC CATGGCCGCG 180
 CCGGCTGCCT CGAACANGCC TTCGTCGTCT ACAGCTTAGC CAGCANCCAA ACCGCACCCA 240
 GAAACCCACA CGCCCGCGCG CCGCGANACC TGCGCCATCG KCTGCTGGGG CGANATCCCC 300
 CGATCGCTNA CANGATGACC GCTGCCGGAA CGCCCGCGGT GCCTCCGGGC AGCCGCGTGG 360
 GCSGGGCAAC CGCGAACCCA NGAACACGGC AAGCAGTATC ANCGCAACAG CAATTGTCAA 420
 GGGCTAAACG CTTACATACC AGGGATCTCG CGGCGCCACA CCGTCGGMTC TGCAGSGCGA 480
 CCCCTCTCTN GGGCGGNCAC TCNTCAAAGA TGCNGATCNA CAGKCTAGGT CTTCGGCCGA 540
 TATGSAAGGN CCCAACGGNT TTAAGCGCGC SAAAAAATC TCCANTGGA TAAATCAGC 600
 CGGGGANCCC CCGGTGSCMM NGTCYCGKCC ATTTNTCAAC MGGTTTNACG GCGGKTGCNG 660
 GCCAACTGCG CAAMTTAAG KTNGGGGNTY CGGGCGGTA ACCGCNNTK NGCCCTTAA 720
 AAAACCGGNA YTTCTKGAT TAMMACCGGN CCCCCAWTGG CGGKTGKTCC CANGNTYAC 780
 AMCTYCCSSS MNGGKGTGGS SAACCCCTCC CGNGGGGTTC NTKGITSYCT AWMCCCCCG 840
 AAACCSKYG GSKTGGCRTN WASSAMNCCC CMNGYTTCTT TAAAGGCCAN KNRAAWGKYT 900
 CCTTGGGAAN CCTNCAATYC GAAAAYYCTC CTYMMGSSCN CTTKWCRTYN NRNGGGAACS 960
 AMWNTYCCNC GWTTCAWTCC GGTCCGASMN AAACKCTTTY TTTYCGSSC STCCMGGSNC 1020
 SGTCKNANAN AAASATTMC YVCNNNANKK YYYCSSGCTT CYKMGRNRNR GMGAACCCGR 1080
 GS 1082

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

AATTGGCAGC AGTGATCGCG CTGAAGCCGG TAGCGCGGGT GGCTCGGGTG GTTTCGCAAC 60
 RAAATCCGCT CGANGTGGTC TCGGTAGCGC GTGTCCANAA CGGTGGCGCG GTGCCGGCGG 120
 ATCTGATCGG CGCGGCGGTA GTGCACGTGC GCGGGCGTGT GCAGTCCGAT GCCGGAATGC 180
 TTGTGTTGTT GGTGTGATCCA GCGGAAGAAC CGGTCCGAGT GCACCCGGGC CGCCTCGATC 240
 GACTCGAACC GTTTCGGGAA ATCGGGCCCG TACTTGAAGG TCTYGAAGTG GGCCTCAGAC 300
 AACGGGTTGT CTTGCTGGTG TGCGGGCGGT AGTGCGACTT GGTGACACCG AAGTCGGCCA 360
 NCANCAATGC CACCGGTTTG GAACATCATCC ACAACCCCGC TCCGCGTMA GTCACTTGT 420
 NCGGCGCTAA TTTNTTGGGC GGCAAGGTTT TGCCGAYCAN KCCGCTCGGC CAAACTTGT 480
 ANTNCSCCA AGGCCNCCAT CCNCCCAAAC AMGTTACGGG ANAAAAATY CAAAGAYCAC 540
 CYTCGGKTN TTATANTCTC CCYTTTGSTY GGGCCCCCN CYTGGKQNA ACCCTNCCA 600

AWTCCCAACN	CCKKCCAANA	RCYKGGGGCC	CCNCCAACC	CGGGKGAACA	WTAATTTAAA	660
CCCYAACMAW	ACTWMMNACC	CNNGGGSCCY	AAMCGTYYNR	AGGTTTTTCT	NAAAGAAASA	720
ANTCGGAAMC	CGGNTSTACC	AAAAASCCCK	CCNWTCCCTC	CRASATTGSC	NCCSAAMKSA	780
AKGCCCCCN	TCSGCNWNCC	CSGCGGKKKT	KKGTTNCCCT	WMRCWMWYTS	GGCCNASCCN	840
CKYYSSMYCC	CCCCCTCCCM	CTCCGNKTC	CCAMCCYANC	MGGCCCCCYTM	GKKCCOCWKNT	900
YKCCCCCCCC	AMNNNNNGGG	WGACCTTNGG	CCCCMKRRGM	TCCCNANTGA	MCCTCWGNRA	960
MKCYCCNRAR	ANMCCSCNCC	NGCNCRCNKN				990

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

AATTCGGGTG	GCAACGCGGG	CCTGTTCCGC	AACGGCGGGG	CCGGTGGTGC	CGGTGGGGCT	60
GGTGGTGGCG	CCGGCGGGCG	GGGCGGTAAC	GCGGGGTGGT	TTGGTCATGG	GGGCGCTGGC	120
GGCGTGGGTG	GTGTANGTGC	GGCCGGGGCC	AACGGTGCTA	CGCCCGGTCA	GGATGGGGCG	180
GCTGGTGTGG	CCGGGTCCGA	CRACRCTCGT	GCCGCTCGTG	CCG		223

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

AATTCGGCAC	GANGCGGCAA	CGGTGGCAGC	GGCGGCACGT	CNGTGGCCAC	CGGGGGGGCC	60
GGGAACGGCG	GTGCGGGCGG	CGCGGGCGGC	GGGGCCGGGG	TGATCGGCAA	CGGCSGCAAC	120
GGCGGCAGTG	CGGGAATGGG	CGATGCCCGG	GGCGGCACCG	GCCTCNGCGG	CATCRGTGGG	180
CTGTTGTTGG	GTTTGGACRG	CGCCAACGCC	CCGGCCACGA	CCAACCCGCT	GCACACCGCG	240
CAGCACAGGC	GTTGGCCGCA	GTCAACGCGC	CCATCCAGGC	CGTGACCGGG	CGCCCCGTGAT	300
CGGCAACGCG	CCAACGGCGC	CCCGGGCAAC	GGGGCCCCCG	GCRGGCACGG	CGGGTGGTTG	360
TTCCGGCGCG	GAAGGAACGG	CGGGTCCGGC	GTACNCRGCG	GGGCGGGCGG	AAATGCCG	418

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

1008432.022502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

AATTCGGCAC	GAGGGGCACG	ATCGCATACA	GCGCTCGCGG	CAGACCCGCC	CGATACAGCA	60
GCTCGGCACA	CGCGAGCGCA	CAATACGGCG	TCTGGCTGTG	CGGCTTGARC	ACCACCGCGT	120
TACCGGCCAC	CAGCGCGGGG	ACCGAGTCGG	ACACCGTAAG	CGTCATGGGG	TAGTTCCACG	180
GCAGATACAG	CCCCACCACG	CCCTTCGGTT	GATAGCACAC	CGTGGTCTTG	CCATATCCCG	240
GCAGCAGCGG	CTGTGCTTCA	CGGGGCTTCA	GCAGGTCCAC	ACAGACTCGT	GCSTTATAAT	300
TNCGCSTTGC	GCGATCAGAT	CGACAATTTT	CTCTTGCGCC	GCCCATCGGG	CTCTGCCCGG	360
CTCGGCTTGC	AGGAAGTCCA	TGAAGAACTC	GCGGTTCTCG	ATNAACAGGT	CGCGATAGCG	420
GCSGATGACT	GCAGCTCGCT	CGATNACGGG	ACCTTCGCCA	GTGCGTCTGC	GCCGCGCGAN	480
CTTCCGCGAA	TGCGCTTCG	ACTTCCGCGG	NCGTGCCAAC	GGAATCNTAT	CACGGGTTCG	540
CGGTTAAAC	TCCTCAATST	NCYGGTCGAA	ATTCCGCAAC	TTCTTATCCC	GGCAGGTGCC	600
AACSANNCAA	ACCTCGGCAA	GGTTAGGMTT	TCCCCNCNTT	YCAAAAATNC	GGKTTTGGGN	660
CMAATTTGCG	CKCNATGKTG	MCAAGGMTCT	CKAANAACKS	GGGTCTCTN	NTCNGKGGAK	720
CCAAAMGGKT	TTGGGGMAGC	GKNMNCAN	CCTWACCCTG	KTKAANGGNW	TTCCCCCGG	780
GGGAKGNGA	ATYCYCCSNA	NCCCRGGGGG	GNMCAATTC	TYCCGGMCTC	CTCKGGAWTC	840
WGMSTTTTCC	CAAAAAACSC	CCCAAATMM	TTTTTCCRCN	TRTTGNACAC	CTTTTKARCA	900
MMCSSAARN	ANMCNCTCYC	CKCTKTGKTK	AAAAAGNAYW	CCCCMAAAT	TYTAWTTSSC	960
CCSCGCGGNN	CCNCNTNTTT	TSCNMTWCTM	WNYTNCRCMC	MMMSNCKNSG	KKGGNRCNCN	1020
CRCCSNCCNM	AAWYNTKGYN	KNTATMAGC				1049

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

AATTCGGCAC	GAGGGAATCG	AGAATCCCGG	AATGGTGAAG	CCTCGGTGCC	TGCCGTTACG	60
CCAAGAKTCA	GGGTGAGCGG	CCCCCGGGT	GGAAATGCTGA	SGCCAACCGG	GAAAGGGGTG	120
AGGGCTGGGG	TGGAATAAGT	GAANGTTACT	GGGATGGAAA	ACCCGGTATT	GATATGTATT	180
GGGCCGATCA	ANGTTGTGGG	AATGGGGGAA	GGGTGAGGGC	GACCTGTGTT	ATTTGGGGAA	240
TTGTYRTGGA	CRAKACWGGC	CAGCCMGCGT	GATGGTTTGG	TTSAANTTTT	GTGCCGSCCA	300
CANGGTGATG	GGATTGATTT	TGATGGGGCC	SATCGAAATA	TGGGGTATGC	CNACGCCSAA	360
CGAGATYGCC	GGGACGTTC	TGGCGGGGAC	AACMASGGT	CCSANGTAAK	GGTTTCCTTN	420
ATNTTGTATC	GGATTCCGGA	ACTMTSTCGA	TGSGCTCSAY	MTSATSGAACC	NACNCCWCCG	480
YTTATTTTMS	GCTNAYGGGA	ATEAMRGGA	CAAYNTCCCT	CCCMGGAAAA	ACCAACMSGC	540
CCTGTGNSYC	CNCCCRCCNC	AKAACCCRTT	KCTGTSTTMC	CCSMAAATNA	CSCCCSCTTS	600
NACTCCNCSG	AANTNSCCCC	CCSCCKNNTT	ATSTYCCCGK	GTTCGCCCMC	CCCTTNAAMC	660
TCCCGCGTTA	AGCCOCWTNT	SNCNCCCCCS	YTAAMNCRG	GCTTSTTNT	CCCCCYTRMK	720
CNCCCGCTTA	SAMCWNCNC	CTCKAACNAC	CCCKCYKSGM	TNCCCAATNT	WCWCKCCNS	780
KTNTTMCCTK	CCAAYTNCRC	CNCNRCCTCC	CKSTSTTCAM	WTATAAACCC	WCWYAWYNNK	840
KCNCMWMTA	MGACWCTCNY	NCCCNCCNCK	NTTKTAMWCC	CKMCCCKCSW	TWCYCKCSGC	900
CMCTCTMAC	CYCCCKCKTY	NKWMCCCTTC	CCCCCCTCCC	MCNMBMKICT	YCSGKTWCWC	960
NCYNTTMTCN	DYNAMCKCK	KTCTCTTCN	CRNTCTCCCC	CCWCCCCCVC	KKCTCTSKCC	1020
CNCCNCTCCS	MMKSGC					1036

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

AATTCGGCAC	GAGATCATGA	ATAGCGGGCT	GGTCAGCACC	GAAGTGGTCG	GCGATCTCGC	60
GAGCAAGTCT	CGTCTGCTCG	CCCAGCAGGA	GGTCGGCACC	GATGCGGACA	CCTGCGATGT	120
CTTGGATGGT	GTTTCAGTTG	AGGTAAGGCC	GACGCCGCAG	CTTGTCTAGC	AGGGTGTCTT	180
GGCTCTTCGC	ACGTGAGGTA	ACCAATAACT	CCGACGCAGA	CCAACCTCCG	CCCTCGATCC	240
GGGTACCAGG	CTCCGCGCGA	GCCAGCCGTT	GTGCCCCCTG	GGCCGAAGGT	CAGCTGCTGT	300
GCGATCGAAG	TAAGAAACCG	CGCCATGCCC	GTGCGCAAGT	ACGACTGACC	GAGCAAAACGA	360
ACGATCGTCG	TCTTTCCGTT	GGGGGTAATC	GANCCAGACA	ACCGCAGCAG	CCACCAATCA	420
TTGGGATTGG	GCCACTGACC	GACCAACCCG	CTGTGCGACA	CCCCAGCGGA	ATTGGTGGTC	480
TTCCGCGGGG	CCGCGNAACG	AATCANCGSG	ACGCGCTCGC	CGAASCANCC	GCATANCCNT	540
ACATANCAAC	GGNNTCTGCG	CCCACATTTT	GGGTTMTGTC	CCCTCNGCAA	CSSNAAYNCC	600
CCCAATTCYG	AACNAAAAAA	TTGGYCCATY	ARNGTYCTCM	CCAAAAACCN	AWTCCCKCTA	660
TCCCCCGGGG	GGGRCGCCYY	NMNAAAACGG	CCCWAAANCC	CCSGGGGSCC	CGGGTTRWTN	720
CCCCCTGTGCG	GCCCNCCSGG	TTTGGTCMCM	GGSCMMTNWN	GGGNTGCSCC	CCCNCAAAAA	780
AAAAAYCKNG	NCAAATYAAA	CCCKYMAAAA	ASKTGGGSSC	CCCMARCCGG	GGKAARKWNA	840
ANTTAANCCN	KAIAAAAAAW	NCANNMCCCC	NGGGNCCTAA	GGKYTTAGGG	GTTSTTNANG	900
ARAAATMTCT	CANAATMNSK	TTNNAAAAAA	ASCCSNWAKC	CCCNNNKKNN	CCAANKAARR	960
SRCTCTCGGG	TTNWSGGGGG	KKKKKTCNMS	KMNMTTWTGR	CCNCCGCCCN	NNTWKCCTTN	1020
TCCNYGGNGC	RNCAGN					1036

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

AATTCGGCAC	GAGTCGATTC	GATCGAACAC	GCCCGCACCT	GGCCAGGCCA	CATGGGCGCG	60
GCCATGGCCA	ACGCTCTACT	GGCCAAACCG	AATCCATTGG	CGCTCTCACC	GCAACCCCCG	120
AAACCGCGCA	CCGCGGCATG	GATCAACCCG	CCACCCCCAG	ATCCGAATAA	GCCTCCACAT	180
AATGAGACAC	TGGCGCAAGG	AGCTTGACAG	CGCGCCGACC	ACGCAAGCTG	TTAGACGTGT	240
CGGTCTTGTA	AGAAGCGGGT	TGGCCACCCA	AGATCACGCC	GCCCAAGGGC	ATCGAGTCAA	300
CGTTGCGGTG	GTATCGCGCT	AACGTCGGCG	CCGCCAAGAA	ATGACGGTGC	GCATTACCAT	360
GGCCCTGCTG	ATCACCTTTG	GCCACCTGCG	CACCANAACT	ATGANCAGCC	TTATGCCGAG	420
TCTCTGTGGC	ATCCGGCAGC	GCTTCAAAAA	CTCCTTGTG	ACAATSGTAT	TGCTGANCAG	480
CCGAATCTTT	NTRCTTGCAA	SAACACTNCA	TGTTNCSGGT	NAACAACCVT	GGTTNGAAAA	540
ACANCCAATA	TTGAANTCCC	ANTCGGGCAM	GAACCCNGTM	CGGAAGKTGK	TGGGAACGAA	600
TGKTGCCCAA	AAATCCCGGG	NGGTRAAAWW	CCCNNSNATG	MSAATTTTSC	CTNGAACCAAM	660
AAAAAGTCCA	AGKYCAAAGG	NGCCCCCCCC	SGNAAATTTG	TGAACSCAKA	WYANRTTCCC	720
WWNTNCAAT	MTTNGGGTTC	KNNTCCCCWT	AAANGGSGCN	CCCCNCCRG	GMGTYTCCCC	780
NWNMGGMGN	CYYSCCCCCA	AAAAAAAMMM	MTTTCGSGKG	SMGGKKCCCC	CCSGGTYYWG	840
GKYYTTAAAC	CCGGKGGGTN	CAAAAAANAN	ACCCCCCAMS	NGGGGGGAAA	ATTTGNAAWT	900

10084843.022502

AAGGKKKTK SCMACCCCAA AAANMMNNCN AwnccCGMGK SARGGGGRNY TIMKAGGGMG 960
 GNYCCCCCW YCGGGGGGNA NAAYAAAGK NGSNGRGAAT NTTNTTTTGK RSSSRNKTIT 1020
 TYNTCTYCN CCNMGNRWWG SRAMNTGKTS NSSGGGSGGC 1060

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

AATTCGGCAC GAGCTTCACC AAAGAGCTGA CATGCCGGGT GATGGGCACAT CGCATCGAGG 60
 GCAATACGGG CATGGATGAN CCGAANGGAN TCTGGCGTTC GCTCAACTGG ATTACGGTTC 120
 CCAAGGTGAA ACGCTTTTGG GCGAAGATG CGACGCTTAA CTTCGCGTTC CACCGTGCAA 180
 TGTNTGATG GATGCTGGAA CCGCGCTGAC NGATAANGAA TTCGCTGGTC GCCGGGCACN 240
 ATSGATGGTC KSTTTTTCNC TCCGCSGTTA AATTGCSTGT GCATCATCTG GCAGGCTATG 300
 TTCCCGCTAC RCTGCAGCCC ATCATGGATG TCGCGCTAAC GAANAAGTTA TGACATGGCG 360
 CAAGCGAMTC GGGGATSCNC GCGGCAMTTT CGCAACCTGC TGTGTNTGAA GCGTMTCAAC 420
 CGAATCGGGC GCTYAAAAGC NGGCTTTCGT TGATTMMAAC CNAACCCNTN CNAITYCTTG 480
 CCGNGNMNTG CGTTCTCTCC AACTCCGKKG SYTGCCNCCG TGAAACCCMA CTNCCCCCCC 540
 GTTGGACTTA MRTNTTCAA AAMCGGMTNA ACCSGAATNN SAACCTNCCR TCAAAANTMM 600
 SAANTCGGGC TTYGGGNRCC CCCCNAAAYW TTCKNCGGG GMNNTYCTCN GTTYNGGCG 660
 SAAACNTTTC CCRTNCMYNN TTTACAMGGC NCMTNMTTGM GGGSCSNNAS GWCCCCGGGKK 720
 TMTTNTCAAW TCNCSKTTT TTKGGGGGGG GGCYGRTRMC NCGGSCCCCC GGCCCKKMAA 780
 AAAAAAMCMA RRCNCYGGG KKCCCCCCCM NNATNGGGCG YKCRAAACAA ACCCCANRA 840
 TNGNGMGGGC SMACCSGNGN GYNAAAGGT TSNCTMANM MKGMANNNCT SGMSCCMNSN 900
 NCTMGGGGT TTKGNNGARN AANAMKMGGM RCGNCGCNN GAAAGGSGMS GSKSCNNNG 960
 NGASNGWMGN CRNNGANRCC NCNGYGNMNN NNGNNNGNNN GGGRIQNAACN NMKMCWMSMC 1020
 NSNMMGNNS CGYMTNKKCG 1040

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

AATTCGGCAC GAGACAANGG CGTGAAATGG GATCCGGCCG AGCTGGGGCC CGTCGTACAG 60
 GACCTGTTTG CCAAGTCGGG GCGCGCGGTT CGGTCATATG GGGCCTAGTT ATCTGCGCCG 120
 AGCGTGAAC TACGGCGGAGA TTTCCGCGCT TTTCTCGCCC TGGCTTCACG TTCGGCGAAG 180
 TCGGGAACGG TCAGGCTTGC CAACACACGA TCGGGATCGT GCGGTTCGCT CAGGACTGGT 240
 ANTCTGATA CTTKGGTACA TCGTGACCAA CTGTGNCNAA TATTGCGGCG GCTCCTCGTC 300
 NGTCGCGTCC CGCGCGGTAA GGTCCANCACT TTCCTTTTTC TCGTGCCG 348

(2) INFORMATION FOR SEQ ID NO:314:

10084943.02502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

```

AATTCCGGCAC GAGAGACCGG GTCTGTTGACC AACGGACGCT TGGGCGCGGG CCCCTTGCCT 60
GGCATCAGCC CTCTCTCTTC TTAGCGCCGT AACGGCTGCG TGCTGTGTTG CGGTTCTTGA 120
CACCTCGCGT ATCCAGCGAA CCGCGGATGA TCTGTAGCG CACACCGAGC AGGTCCTTCA 180
CCCGGCCGCC GCGCACCAGC ACCATCGAGT GCTCCTGCAG GTTGTGGCCC TCGCCGGGAA 240
TGTAGCGCGT GACCTCGAAC TGA CTCTGCTCA CTTCACGCG GCAACCTTCC GAACGCGCGA 300
GTTCCGGCTTC TTCGGAGTGG TGGCTCGTGC CG 332

```

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

```

AATTCCGGCAC RAGTCGGTCT AGACGGATTCT AATGCTCCCG CGAGCACCTC GCCACTGCAC 60
ACCCTGCAGC AAAATGTGCT CAATGTGGTG AACGAGCCCT TCCAGACGCT CACCGGCCGC 120
CCGCTGATCG GCAACGGCGC CAACGGGACT CCTGGAACCG GGGCTGACGC GGGGCGCGCG 180
GGTGCGCTTT CGGCAACGGC GGCAACGGCG GGTCCGGGGC GAACGGAACC AACCGCGGGG 240
ACGTGGGGAC GCGCCCCGGC GGATTCTTTC GCACCGGSGC ACCGGCGGGG CCGGCGCGCT 300
CGCACAAACG CACCGGCGGG GACGCNCGCG CCGTNGGGCG GCTTCTKGAT GGGCTCCGGC 360
GGTNACGGCG CACGGCGGCG CCGGCTCAC CGCCNGTTGG GACGCGGGGA CGCGTNACCC 420
CGATCTTCTT CCGCNCCCCG GAAACCGCGG GGCCGCGCCC ACATTAKACC CGGCGGNACC 480
GCGGMCCECG CGGAACGGNG GGYNTTTTCC AACGGCGGGG CCGCGGAACC GNMGGSTGTT 540
CCTTNGGSGA AGGNCCAAKT CCCGKCTANC YYAATCCCCG ANGSKTGAMC CTSATGSNCA 600
MYTTMAGGAA CYTNCCANT KTTSGRACW CRCNNGGAAA ASRAWNKNGT KGGCAACNA 660
NNTNCTYTKN NATTKGGNNA AAAANCCCTY CCWCSGRACT NCCCCCNMG GRMCMNNTNN 720
NTTTYGCNHN CCGGGSNAAM RNTTKATTTC NGGGGNGTCN GGGTKMNNNA AACCCCAAA 780
MNRNKKSCSA ANGGGKSNGC NKNMNMNSGT TTTYCKNMRA MRNWTYKKNK NTCNGARSRN 840
NAAMCNSNKN NGKKKKNKAA ARNNTTWKTN KNSCNKNCN GRNRNGVGGC CKMKGSNMNG 900
MCWHNAWRNG NNGSNCNCKC NKNMNAAAAA AASGGVNCKS NSMKNKKKKG NRRGGGGGGG 960
GG

```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10084843.022502

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AATTCGGCAC	RAGAAGACGC	COGAANGTTT	GCGCTGGCTC	TACAACTTCA	TCAARGCGCA	60
GGGGGAACGC	AACTTCGGCA	AGATCTACGT	TCGCTTCCCC	GAAGCGGTCT	CGATGCGCCA	120
GTACCTCGCG	GCACCGCACG	GCGAGCTGAC	CCAGGATCCG	GCCGCGAAAC	GGCTTGC GTT	180
GCAGAAGATG	TCGTTTCGAGG	TGGCCTGGAG	GATTTTGCAN	GCGACGCNCG	TGACCGCGAC	240
GGGTTTKGTG	TCCGCACTGC	TGCTCACCAC	CCGCGGCACC	GCGTTGACCT	CGACACAGCTG	300
CACCACTCGT	GCGCTCTGCTG	CCG				323

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AATTCGCAGT	GTGTGTGGCG	GCGTCCAGAA	GAAGATGATC	GCGAACATCG	CCAGCGCCGG	60
CCAGGCTATG	GTGCCGGTGA	TGGCCGACCA	GCCGATCATC	ACCGGCATAC	AGCCGGCCGC	120
CCCACCCAC	ACCACGTTCT	GTGACGTGCG	TCGCTTGAGC	CAAAGCGTGT	AGACRAACAC	180
ATAAAACGGC	ACGGTGACCA	GGGCCAGCAC	CCCCGCCAGC	AGGTTCTGTTG	CGCACCATAG	240
CCAGAAGAAC	GAGATCACCG	TCNACGTAC	CCGAGTGCCA	ACGCGTTTCG	GGTCGGCACC	300
GCTTCCCGCG	CCAAGGGCCG	GCGCGCGGTT	CGCTTCATCA	CCTTGTCGAT	ATCGGCGTCG	360
GCNACCAGTT	GAGCGTGTGT	GCGCCGGCCG	CSGCCATCAT	CCCGCCGACN	ANCGTGTGTA	420
GCATGANACG	CGGATGAATG	GCGCCGCGCG	TCGTGCCGCT	CGTGCCGAAT	TCAACTCCGT	480
CNACAACCTT	CGGNCGCACT	CGAACCCGGG	TGAATGAWTG	AATTTAAACC	GSTSAACANT	540
AACTACATAA	CCCTTGGGGG	CTCTTAACCG	GTYTGAANG	GGTTTTTTCG	TTAAAGGAAG	600
AACYAITTC	GGATANCCTG	CSTTNWTARC	GAAAAGGCC	CRCCCATNGC	CCTCCACAGT	660
TTSCCCCTGA	ATGGSAATGG	MNCCNCCYKNR	CNGGNCCTTT	AACRCGSGCG	GGMTTTTGKT	720
MCCCNCTKA	CNTTMMTGC	ARNNCNGGCC	SKCCCTTCCK	TNTYCCCTCC	NTCCCCCNST	780
TNCNGKTC	CNNAMNYTN	ACGGGGGGCC	YTNGGGKCRM	TWTKKTTTGG	GCCCCMCCCY	840
MAAANASAA	GGGGKRNCTY	CSTTTGGCNC	CCCAMAARGG	NYCCCCCCAM	YTNRRKMCST	900
CNNTNKGNN	CTGTNCKNCG	GAARAMAMCC	KCCCCGNSTS	STTNGTYWAG	GNRWKGNRSR	960
CCSCCCCGGY	MNNNAAYAWN	WMNATNCNNS	STNANMAKKN	NNNNNNNSCN	WNGWGNNTCN	1020
SCNSNGKBC	CSCC					1034

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

AATTGCGCAC	GAGCCCACAT	CGGGGCGCG	TCGTTGCATG	ACTCGTTCGT	CATCGTCGAC	60
RAGGCACAGT	CGCTGGAGCG	CAATGTGTTG	CTGACCGTGC	TGTCGCCGTT	GGGGACCGGT	120
TCCCGGGTGG	TGTTGACCCA	CGACATCGCC	CAGCGCGACA	ACCTGCGGGT	CGGCGGCCAC	180
GACGGGTGCG	CGCGGTGATC	GAGAAGCTCA	AAGGTCTATC	GTGTGTCGCC	CACATCACCT	240
TGCTGCGCAG	TGAGCGCTCG	CCGATCGCCG	CGTGGTCCAC	GAGATGCTCG	ANGAGATCAC	300
CGGGCCGCGC	TGAGTGCGCC	TCCCGCGAGC	A	-		331

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

AATTGCGCAC	GAGATCGTCA	CCCTGGCGAC	CAGTGCACCC	AGGCCACGCC	ACCAGTTACG	60
GCTGATGGGC	CAGAAGATGG	ACCAGGTGCT	GCCCATCCCG	CCCACCGCAC	TGCAGCTGAG	120
CACCGGGATC	CGCGTCTCTA	GCTACGGCGA	TRAGCTGGTG	TTCGGCATCA	CCGCTGACTA	180
TGACGCCCGC	TCCGAATATC	AGCAGCTGGT	CAACGGTATC	GAACTGGGGT	TGGCGGCTCT	240
GGTGGCGCTC	ANGACAATT	CCGTGCTGCT	GTTTACAAGG	ATCGGCSTAA	CGCTTCATCC	300
CGCGCACTCC	CCANCGCCGC	GCGGCSGGGG	CGGCCCTCTG	TGCCGACCCG	CCGAGCGCGT	360
CACGTACGCC	ATCTCCGTGC	CGGTTAAACC	CGTGAGAAGG	TGGGTCTGTC	GCAAGTTGGG	420
CCCGGTCAAC	ATCNATCCGC	GCGGCCATGA	CGCNGTGTCT	TTCACACCA	CNTSNGACNC	480
CCCCAGGAA	CTGGTCCGCG	AMTNCAGGAA	NTYCGTGTGG	GCACNCGCTT	CTTCCGKTRT	540
GGCYTAACT	TCCNATSTTN	CSGCSGGCCT	CTGGCGTTNC	GNCCGGGCGC	NTCTTNCCAA	600
ATCGGSMMAA	ATCCCCANMC	AAACCCCGCG	GGTCTTGS GG	GCSGGGNGGC	GGCCNAWNCC	660
AAACCCCGCC	NTTAAANTCT	TTGKTNCCNN	CNCSGGCNCC	NCNAANSCAN	CCCTTTKGGC	720
NCTTCCCGCC	CCCAWTTTAA	CCGAKCGSCN	AAYCCCAAGY	TMMGKCCYCY	KNAAAAAATA	780
AATTGSCSG	CCCCAANTAA	ATTCCNNGGC	CCYTTGGGGG	CGRANCNNT	TTTMCSSNS	840
TKGNNAAMC	NGGANCCSGG	KAAATMMTKG	NAAYCGCCSN	AAMBNTTTTC	TAANNCCCN	900
YNCCCSGAA	ATTNNAMAAM	CMNNKTGNSG	GGGKTTSN	SGKKGRAGGM	AAAAAANRSN	960
SKTTNMCNN	SANMNCNSNN	SGGNSNNNNN	NNNCNCGYKC	CSNAANMCCC	CGCGGGGGGG	1020
CCMMCC						1026

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

AATTGCGCAC	GAGAAGACGC	CCGARNGTST	GCGCTGGCTC	TACAACTTCA	TCAARGCGCA	60
NGGGGAACGC	AACCTCGGCA	AGATCTACGT	TGCTTCCCG	GAAGCGGTCT	CGATGCGCCA	120
GTACCTCGGC	GCACCGCAGC	GCGAGCTGAC	CCAGGATCCG	GCCGCGAAAC	GCGTTGCGTT	180
GCAGAAGATG	TCGTTGAGGG	TGGCCTGGAN	GATTTTGCAN	GCGACGCCNG	TNACCGCGAC	240
GGGTTTGTGT	TCCGCACTGC	TGCTCACACC	CCGCSGCACC	GCGTTGACGC	TCGACCAGCT	300

10084843.022502

GCACCACTCG TGCCGCTCGT GCCG

324

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

```

AATTCGGCAC  GANGCGTGCC  GCTNAACACC  AGCCCGCGGC  TGCCAGATAT  CCCGGACTCG      60
GTAGTGGCCG  CGGTGGCGTC  GTTGCTCTCC  TGACGGGGCG  CGGCGACCAT  AAGGTCGCTM     120
ATGCCCAGGT  AGCGGCCAGG  GTGCATGGAG  TCGATGATGA  TGCGACTCTC  CAGCTCGCCG     180
ACCGGGAGCT  TGGCATCGGG  CTTGATCAGC  CAGGACGCGT  AGGACAAGTC  GATCGAATGC     240
ATAGTGGCCT  CCAGAGTGGC  CGTGCAATTC  CNGCGTGCTC  CACGGCAAAAT  GCCTTGATT      300
CTACTCCGCG  TANTGTTCCC  GCATCGCCTG  CGGGATGAAT  GGGAACCGCA  SGATGGCGAC     360
GAACGGGTCT  GANCTCAGT  TTGCCGCTTT  GCGCACAGTG  GTCNACANCC  GGTACTCGCG     420
ATANATCTGG  CACCNAAATCG  GCGCCGACGG  CGCCACACAT  AANAACGGGC  ACNACAATCG     480
CCGCCCGGCT  CACCNAAACA  ACANCTTGSC  ATCGGATTTT  GTCCCCANGC  CTCANCCGT      540
CCCGAAGGCC  TCNTCCGGCG  NACTTTTCTT  NNAWTAACGT  CCGCTTCCGK  CCCTGGNGCA     600
WTAATGGGA  AACCTTNC  CCACCTTGAA  GGGTTGTTG  NATTTTACT  GSTAACCCCG     660
AATTTTCCG  GANTCGGTGN  KCCGGGTTT  YSTNTTCCC  ACCTTNGNAN  GGGCCGGCCA     720
AGSTTTTCTT  SYTGAAGGCG  GAAACCCAA  TTTNTYTYN  AACCSMNAA  MYMTTTCYSG     780
MNAASCNKT  CCCCCTTAA  CAMGGSGTN  AACCGKTMNG  NGGKTAAAA  GGGSKNNKTG     840
NCCCYMANG  GGGGGRAAA  TSTKTCNNG  GGGCKAAA  ACCMMMYGN  GTGKKKNS      900
GCSAAATTT  NMMRAACTN  GGGGCCSSG  NNTTTNAA  MSCCCCSNN  GSTGKCCCN     960
NTTTCNNAA  WMKKGKWNM  SNMNSCSNG  GKYNSSGNN  NNAAGMGGG  1010

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(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

```

AATTCGGCAC  GANGCGTGCC  GCTNAACACC  AGCCCGCGGC  TGCCAGATAT  CCCGGACTCG      60
GTAGTGGCCG  CGGTGGCGTC  GTTGCTCTCC  TGACGGGGCG  CGGCGACCAT  AAGGTCGCTM     120
ATGCCCAGGT  AGCGGCCAGG  GTGCATGGAG  TCGATGATGA  TGCGACTCTC  CAGCTCGCCG     180
ACCGGGAGCT  TGGCATCGGG  CTTGATCAGC  CAGGACGCGT  AGGACAAGTC  GATCGAATGC     240
ATAGTGGCCT  CCAGAGTGGC  CGTGCAATTC  CNGCGTGCTC  CACGGCAAAAT  GCCTTGATT      300
CTACTCCGCG  TANTGTTCCC  GCATCGCCTG  CGGGATGAAT  GGGAACCGCA  SGATGGCGAC     360
GAACGGGTCT  GANCTCAGT  TTGCCGCTTT  GCGCACAGTG  GTCNACANCC  GGTACTCGCG     420
ATANATCTGG  CACCNAAATCG  GCGCCGACGG  CGCCACACAT  AANAACGGGC  ACNACAATCG     480
CCGCCCGGCT  CACCNAAACA  ACANCTTGSC  ATCGGATTTT  GTCCCCANGC  CTCANCCGT      540
CCCGAAGGCC  TCNTCCGGCG  NACTTTTCTT  NNAWTAACGT  CCGCTTCCGK  CCCTGGNGCA     600
WTAATGGGA  AACCTTNC  CCACCTTGAA  GGGTTGTTG  NATTTTACT  GSTAACCCCG     660

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AATTNTTCGG GANTCGGTCTN KCCGGGGSTTT YSTNTTCCCC ACCTTNGNAN GGGCCGGCCA 720
 AGSTTTTCTT SYTGAAGGGG GAAACCCAAC TTNTTYTYYN AACCSCMNAA MYMTTTYCSG 780
 MNAASCNKNT CCCCTTTAAC CAMGGSGGTN AACCGKTMNG NGGKTAAGAA GGGSKNNKTG 840
 NCCCCYMANG GGGGGRAAAA TSTKTCNNCG GGGCCKAAAW ACCMMMYGN GTGKKKNKSS 900
 GCSAAATTTT MMRAACTFKN GGGGCCSSGA NNTTTNAAAG MSCCCCCSNN GSTGKCCCN 960
 NTTTCCNAA WMKKGKNNNM SNMNSCSNGG GKYNSGGSN NNAAGMGGGG 1010

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

NGNGGGGWS NTCAYCAYCA YCACSGGGY CWATTGCGGC CGCAWCTTGT MAASAGATCT 60
 CGAAYTCGGC AMGAGGGAMT CKCTMGCNCC GCTGTGCAAN CCAATRAGGC CTRATAATTY 120
 CCACTCCACA AAAAACCCTT GTGTGTAYYT SCCGRAAATR AAGGCGCCGG TMTCAACWYC 180
 GCCGGTCTTY CCRATYCCCG TKTTGTAMCT GCCKGGGTSR AAAYCCCCGG TGTGGAYCC 240
 CCGGATTGAA ACTGCGCGGT TGAACATGCC GKTTSGCSA TCCGGKWAT GAMSTCRCCG 300
 ATTAAGAAAC CGGKKTGGN GCTGSNCGTG CCAATNCGR AYCCRTATAY CCAATGCGCTG 360
 KYCTYCTCCK YCGGTACCCA AAYCTGGGTA TCCTATACCT GYCCCTAAAK GCAAWYCKGG 420
 GCTGYCNMTK TTGCKGSGGT CCNAATTAS CACCAACGCT TCCTTCCATA CCNAACNCG 480
 CKTGGGCWCC AGMCCGRAAA AAKAATAAT RAKAAKGGTG CATNYCCAAA ACCNCCGCN 540
 CCCNANTNEN ATCCGNTNCC MSCNCCCCCA GCGGTNAAGK TKSGGAAATT CTMMAACCCC 600
 CAAANCCCCA TAACNTNCGR GAASAAACCC CTYCNCGGGG GYCNWNCAAA ACASCTNTAT 660
 TTGCTKSTTT CGGGMCCCGT GCCGCCNAAA YCCCAAASTA CTTTYTGGGT CCNAGAKAAA 720
 ACCNCGGGCN CMCNCCSNA NWTATYCTT KGGCAANCC CSAAACCTTR CTMNAACCNK 780
 ATRMTCCCTT CCCCVCAT TGGYCGGRAT NCGSNCCYTY TCAAAKKKSC CAKWNNNGG 840
 GRNNACMA ACCCCAAGTY CCMNAAAATN GKCCCGCTC CNAACACGNK TTYTCCSAAA 900
 ASCCCWCCCC CCCCCCRAA AACCCCCNCA RKANTNCCCA AAAACNYNGK GGCCCCCCCC 960
 CAAACMAAAA AMCCCCSGM RMACSGGGGN NMCCCGKKK KRTTTTCTT TKCCMRSCCC 1020
 AAMGCMWSY KSKTNMAAAA GGAAGRANCN TYCCSANANM TCCCNWRSW CCGSWGNGNA 1080
 GAASMCCCC CS 1092

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GGGGGGGNNN NATACATCWT CYGTGYACCG GGGMTCTAKT GCGGGGCGGC AATCTNGTCA 60
 ASAGATCTCT NAMTTCCGGG ACACAAACTT GACAAASYMT CGNGCNMTCC GTGTCTCNKA 120
 TCGCAAAACG NGTRACASAC ASACACRTAT GTGTGCCAC CASCAAYTCK TTGGGACCTC 180
 GCTRACCCGY TGCCCRNACG CCACGYTGCS CWTCTATCCC RACGCCGGCC ACGGYGGGG 240

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ATATTCCAGG	CACCACGCC	AGTTTGGTGG	ACAAATGCCCT	GGCAKTTTCC	TCRAANTTCG	300
TGAAACCGAA	TTCNSMTTGA	ACNCCAAARG	CCCCSNCCNR	AACARTTGGG	WTCCCGGGTT	360
CTCCCCACCG	KTTTCCGGGG	GTNTCCGGCAN	AANCGCACCC	WTGGWTTCTM	TCNCCGCACC	420
GGGCGGACAA	NTCGGGTTGC	AATTTTGCR	AYCGGGGCG	GGATTCCSCA	AACGGGTGCC	480
GAAACTGTGY	YCRAMACCG	GGAKCCGCAA	TTTCCGGGCR	ANAAATTTCN	YCNACCACT	540
GCTTTRACTT	CCCCGACCGT	AACMANITTC	ATCTCTNTNN	CCTCTGCGCT	TGGGCGAGGG	600
CKAAAYACCG	CMTTTGGTTT	CGCAACCTGC	GGCCCAANTC	CCNAMCCRCA	CTTTTCAATT	660
GGNTCGAATT	SCCCCCCGGT	RANAACCSCC	NTGGCCNNYT	CGGASSAAAA	NGGGCCCTNT	720
KGCCNSCCCC	AGTAANACCC	TACCNAYTS	CAWTCTTTGC	CAAASITKGG	ACGAANSKTG	780
GGNTTCCGGK	ATTTTYTTGS	GGNCNCCTTN	TATNGGSNTN	GGGCCCKCYN	NCSTKTGKCA	840
NASSKAYCCS	NGNKGGGGGT	ACCCCCCTMG	GGGGGTTTTT	NSSGCCCCCC	AWAYGNKSTG	900
GCCCCNNNGG	GGAAKAATWT	MWWTMCNSGG	GGGAATTTTT	NTSTGGAMCS	SGGACYCCCR	960
GGGGGKTTTT	TCCCCNCNSA	NNAWANGGGG	GGGGGANAYT	NTGNSGNGGG	KWNTTTATTT	1020
YTTYCYCCTM	TKACMSGGGG	GTTTCKAKNG	GGGGGAGAAA	ANAAAAAANA	RAKGGYKNTY	1080
TSKNKACNCT	GKWNWNWANR	NAGAGTKCCT	CKKCCNCNSG	SNITTTCTTT	MGNSGSGYGG	1140
GNNGNNNAAA	ACNKSRRMAC	KCSYTYCCCG	CGYCTCTCCT	NCNCGGGYGS	NGSCGNSTYN	1200
GNNKGRKWT	TNMTGNCGTN	SCCTCCNCCC	GCKNKNGTGC	TMTCNMYGSG	C	1251

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

AAYTCGGCAC	MGAGTATCAC	CAAKCTGYGT	GGCCCAGCAA	AGTGGAGCTA	TTACTACCTG	60
TATGTGATCC	TCRACATCTY	CTCCCGCTAC	KTGGTCGGGT	GGATGGTGGC	CTCGCKTGAK	120
TCRAAGGTCT	TGGCCRAACG	GCTGATCGCG	CAAACCTTTG	CGCCACGAC	ATCAKCGCCG	180
AACAGCTGAC	CTGCMCGCCG	ACCGGGGGYC	GNCAATAACT	CCAAACCGGT	GGCMCTGCTG	240
CTGGCCNACY	CCGTGTCCCA	ANTCGAACTC	ASCCSGCNMA	CCAKMAACKA	NAACCGTTGT	300
CTGAAGCCCA	GTTCAAAGAC	CTCAAGTWCC	GGCCCRACCT	CCCGAAACGG	TNCGAGTCKA	360
TCRSAGGSGG	CCGGGTGCMC	TGCAACCGGT	TCTTCGGNTG	GTRCAMCCCN	AAAMCAAGCA	420
TTCCGGGTC	CGMMTGCCCA	CGCCGCCAAS	TTTMTCTACG	CGSGSCCNAT	CAAATTCGCC	480
GGGAACSGSN	CCMCKCTCNK	GGAMACGCCC	TWCCAAAACC	CYCGAACGGK	ATCCTTCKGY	540
NAACNCCCGA	RCNCCCKSKT	TCGGGGCTTC	NMSGCGAATA	CCCKNSCMNT	CCGAATCCAA	600
TTCCCMKYGG	CTTTTYYVCC	CCCCGGCCCC	AAAYNGGGYC	CCTASSNMKC	KNCCAMNANT	660
CCNWTCTCGG	NGGTCCCNAN	KYYGGCGTTC	NMAATSAMNA	NMNRGGGTYT	TSYACCCMMN	720
AACCGKNKNG	KCCCKMCKTK	MANAAAKATT	RATCAMKWNG	GGNKCKCNEN	NAAMACCCSN	780
CNCYNCWYTC	TMYSCKGWGC	GCSMYNANCA	SNGGGGAGGW	GGSGRMKMTK	CTMTCTCNCT	840
MGCGCCKNTN	TYCKSGAKAT	ACASMNKTCC	GCGCMGCGCN	MAAMANRAKA	CTAKCCGYGN	900
CCSNSTMYTN	CTSNNMKNMN	TCCWMWNATC	NTYYGKKCN	KCTMKATNWC	CSGTSKCNCK	960
MRAMTCKTYG	SNMTCTCTCA	TCNCTCKKSC	SNMSKNTCKC	KSCNCCNCWN	CNCKNMKCNW	1020
GGNSTCRCCY	TCTMNNNTCS	AGCKCGSKNC	WACNCAACAK	NGCWCTYTTC	WKNNMKCNKM	1080
TCKCKCACRG	MTMTWCNCS					1099

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid

202507.244843.1008437

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GNGNTATACA	TCWCCTGTGYA	CCSAGGATCW	ANTGCGGCCG	MAAKCTWSTM	CASAGATCTC	60
AAAYTCTGCA	MGAGCGGCAC	AKAKYSTCGT	CCMRACCCGG	CAYACWCCWG	CNCGCCCCWT	120
CTTRGACCGG	GGCKATAMSC	ACCGTTGGCC	CCGGCNCGCA	CCTACACCAC	CCACGCCGCC	180
AGCGCCCCCW	TRAMCAAAAC	ACCCCGCKTT	TACCGCCCGC	GCCGCGGGGG	CCACCACCAG	240
CCCCACCGGC	ACCACCGGCG	CCGCCGTTGC	CAAAACAGGC	CCGCKTTTGC	CACCCA	296

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

NGNGSGNKMY	ATCATCWTTT	TGCACCSNNG	MTCWATTGCG	GCCGCAATCT	TSTMNASAGA	60
TCTCGAAYTC	GGCAGMARCA	TCTGCGCGGN	GAATGTCCAA	AWGTCWKTA	CGGCMATCGG	120
TTTGCCGYCA	ACCACKCTRT	SCAKATGCGG	GCCAMWYTC	AACCRATTAT	TTGGGYCGAG	180
AAAAATTTMC	CKTGTRASCA	ACCTGCAGCG	GGTCAASCAA	CAGCCTCTRA	ACCGTAAATY	240
CKTAGGTNKT	YCCGGCAACA	ASCYCRATAA	TSCGGCCCGC	AMCCACAAAA	CCTGANINGT	300
TNNTTCNCRA	NCCGGTYCCC	GRAGGGGTS	ACTGCSGTAR	GCTTNTCWYC	NCCTTRACAT	360
TAAACCCCCC	CGGNTCWTCG	CCGCGCCCAA	ATYCYTGCCC	WTKGCNACCA	YCCCANCCCT	420
CSGTATGGTS	RAANCASTSG	GCRAACGGTM	MCCSTACCKC	TGGCTGATYC	KTCGGNTCCS	480
SNAATTCGGG	GATTTACGGS	CAMGGTTAAY	CCAGGYCCCC	TNTGCTYCKY	CNAGAACCSCG	540
ATCMWCNCCG	TACCTKTTAA	AATTCITTTGT	GGTGGAAACC	AWYCKAAAA	NMTINTYCCCN	600
TCCAMMGGGG	CYCGGAARKT	CNACNTGGKT	NACCCCTNCC	YTTGAASTTT	TCYTGNCCCC	660
GGCCCKAAAS	ANACCSGAKC	CCCGGAAYCS	WTAGGCYTCN	TGCCCCSTTA	AATTKGNCYC	720
AATCKKCCAA	CGCTCCCCGG	GGTCSGCCMT	TAAAMTCCOC	CCCKSCASNG	GAATYCYKSG	780
GCWGTMTATT	CNCCCNNTTT	CYYGKNAAAC	SCCCCCWKG	GSCTYCCCCN	SNITSSGCCS	840
GGTTS GAMYC	AAAANTNGGG	MMCNRAAGCN	SGNAMCCSCN	GKKGGSATW	TKAAYYCYGG	900
GGGGGTTCNY	CCCCRCSNAA	AAGYGTGKGC	KCCSSSCCYC	CKMARTTYYT	CNGGMRMAM	960
ACCAAGGGNG	CTCCCGTNCW	WGGCTCCCSN	SNSMAMAAAN	NKCKCKCKGS	CKGARRNMNA	1020
MCTCSNGNGG	WTCCCKNKTC	NSCNSGNCGS	YGGNSASWCC	YNYCNCCACA	ANC	1073

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

10084947-02502

CGCCCGGTTTCT TTTMMTTTCAY TCATTACCCG GGMTCTAGTG CGGCCGCAAK CTTGTCKACA 60
 GATCTCGAAY TCGGCAMGAS ACAATSTCGG GTKGGGCAAT GTCCNGTGGG GCAACTTTGG 120
 GCTCGGGAAT YCGGGGTTAA CGCCGGGTCT RATGGGTSTG GGTAATATCG GGTTTGGTAA 180
 TGCCGCGCAGC TACAAATTCG GTTTGGCAAA ATATGGGTGT GGGCAATATN GGGTYCGCTA 240
 ACACCGSCAS TGGAATTTVC GGTATTSGGT NACCGGTTRAY AAYCTGACCG GGTNCGGTGG 300
 TTYCAATACC GGTAACGGGA ATGTSGGTTS YYYACYCCGS GSAACGNNWW YTTNGKTCCT 360
 TMMCNCTSSM CCKSAAMTSM KMGGTSTYCT MTCNNNGAS TAMTYNMCCC CCGWAYCKSC 420
 WAYCCCTCGT CATYCCMC MC SSGSYCCTCA MNCCACCYTG NGYVCCTTCC MKMTICYCAYT 480
 CMNTCCGGTW CCTNTMMNC CSCNCRYCTC AMCNCTKSGK CACCNATMYC CSACKCHTCT 540
 MCYMCSCAKN MTTCCTCTCN CCTYTNCCA MCMCSTCTM TCMAACTCKC CCGGYCKCNC 600
 MYCTCTCKTC AYNNMAACCK TYCYWNCWYC YMYCKCKCAG WYKNMCTCCW ACTCTMYNTT 660
 TCTCTCNKCC CMKACCKNTT CTCWCSCCCC CCACAKAYMC YAWCMTMTCC MCTCKACSCC 720
 CYCYNNYCCM NMCWMTCTWC TWNAKCANCN TCTTCTCTC MMYMTMACKC WCNNTCNCKC 780
 SGACCYTCTC ACTKMKCKCM TCTCCTTMCX CCYMWNCNCC MKYNCCCTCC NMTCTMCKYT 840
 CCTCNCMRY CYYYAKCAK NMCTCCCCAN KMAKCTKCT CCCCCKMKMS ACNCKCCCWC 900
 CCTCCTATCC WCTCTCTCTC ATCTCKCTCW CNYCMYMKMC ACNCKCYAYT CNACTMMNWN 960
 CCANCNCTCT CTNYCTCWCK ACGTYCKCKC CTMCKCNMYC NRWCTYRCCT CKKCCNCRN 1020
 KKNMCMCKMT CTCTCCWMKM TCCCWCCCAT CTMMKSTCTC WCNMCTCCCT CKKCCNCRN 1080
 KCYTYCCMYG CTTCNCTMMK MCCWCCYATC TCTMKCTCTC CWCACMYCAC WMTTACWNCC 1140
 ACTCTCTRCW CKCKCKMCCR MTCTCB 1166

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

NGNNGNNNTT CWTACATCWN TCTNACCCSG NGMTFCWATTG CGCGCCGCAW NCTTGTMNAS 60
 AGAATCTCNN AAYTCGGCAC ANATGCTTTT TSTMTAKTGT GCGGGGGNGC CACGCKCTAT 120
 GTGYGCTTGG GYTRACCCAA CCCCGCGGCS CGGGCCRCAC AGGCGGGGGA TSCAGGCCGC 180
 GCGCGCCGCG CGGGYTATAT RAAGCGCCGY TTTTKTRATA AAGCTAATT GCAACCAWTT TTTYCGGGTC 300
 TTAGCGGCAA AAYCGGKRTT TTGGGTRTAT AACGCTAATT GCAACCAWTT TTTYCGGGTC 360
 AAAAAACCGG CGWGCANATC NCGGGYCNCT RAGGCGCATG YMGCCCAAAA WMTTGGGCGC 420
 AAAAAACCGG TSYTATTPTN TGGGCTATSC GGYTGCTTCG GCAAAACGCTY CCGCGGTTAA 480
 TCCCTCTCCG CGGCGCCGCN AAAAAACCA CAAATYCGYT GGGGTGKYCC CMCAAGGCSGT 540
 TGCTYCGWGY CACTTGGCCA AAYYCCAWT AKATTGGGTG SCYKTCSCGG TTSYTGGGCY 600
 CAATTACCCC CNGCGGNAAA GRRAAANAAT ATCNTCCNNT TGCTCGGYCA YCTTMTTGG 660
 SAAAGGGGCG ATGGCCCGGT TYTTTACTT CAAYCCCCNA NCANTWACCT YTCSCCCGCG 720
 GGGGNCANAA CGSTTNGCTC CGSGGNAKCC TKGTMCCCGN ATCNAAAGGC CNGAATTGG 780
 TTYSTYCNAA ATWTTWKKKY CCCCWNTTG YAAAAACCA AAAAAACCC YCNCAAMMYKT 840
 NGGGGTYSGG GCCKNYCTTK SNMTTAAACC CYCCCCAAAA YNNSGGGKKT TCCGCGNSAT 900
 KCCACCNCKK GNNGGGGNA SAAAAAAY TTYCCSAAA ATCCCACTY TCKYTKSTRY 960
 AMACCCCTCT TYYMKAYTC KYSCNATTC SGMTCNAWAA TYCCGYGGCT TMTTCCCKC 1020
 CCGGNGCCCT AAWTTTGT TYNCAANTTY CCNAAMNMC AWTMGGGGS KCCATTCTCG 1080
 SCYTMANANA AANAANAGGG NKTTTYYCTY MANAACAACN GTKGCNCCN CNAAMAAAN 1140
 AKMAAAKAGN KKKMTNNNSA AANCCNCCCC CTSTYNTYT NKTNNMCKCC CYGKKNTKGM 1200
 SWSYNTTCT NCCCRCCCC YNNTKTGANA AAMNCCYCCS GGSTMCNAN ANMNTTCTCK 1260
 STSTNGMGCC KMBASNANAN MCAMWKWYCC

10084843.022502

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

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NGNGGGKNNNA TMAYCWTCTC ACSSGGTCTA TCGGCGCAW CTMGTMMAASA GATCTCNAAY      60
TCGGCAGNNAN GCATMTCMMC CATATATAAC CATTGCGTCS GYWTGCAWCT CRAAWCTGTC      120
CTTCSKCGCC TTKTACRAAG GTGGMWGTGT CWTYCCTRAA SCCCTCRATC TCKTKTATYC      180
KITGCGGCTCY ACTTTAACSG RATKSCGTGCC TTKTAYCAAT RATGCAAWTA WTGGYVRAWT      240
CTKGAGGCGC RACGGCWYCT TTTYCCGCRA GRACAATNGA TTGGAWYCGC TYCGCRAGGC      300
CCGGCACCARR ACCGGGCNCC AAAGGYCCGC GCAAWTSCCT GGKTCAAAAA TGGTGCAAAAC      360
AAAMCNATCC CCGGYTTRAC CGCAGYTAMC ACAAKAAAAA TCCCTWGGCC GCACCAWNTT      420
TTYCRATCWY CWYCCCCACC TTRAACCTGK YTGCSGTATT GCCTKCTGCG CTCRACAGCM      480
YCNCCKCTCA AACCTGCGGT GACTCCAAC TGGTCTGGYCG AASGGGGGYT CAMCGGACAA      540
AACCCCRANN TCGCCAAATT TTCNCCCCC CYCGGGAAN GKTGATMTTC TCSNAACCSA      600
CMGGGNNYTW NAACCTCGAA CSSSGSNKGA MYNSCCSGGA ANTTTTCCCT TYNGGGCGRN      660
AAANCCCTTT AAGGTACCCC KGGNGGGKGG CCCYTTTGGG AAAACAACCC CKATTGGKTT      720
TGGAAATNTT TKCNCCCCCA TTCNSGGGGG GGGCCCCAMC CCMCTTTTN TCMSCNMTYY      780
YCYVGGGAAT TNYTCCGCSG GAAYVCGGSM CCKGYCCTAA NCCCCMNWGG GKYSTGSNAR      840
GGRAIMAWWT TYSTTTYMYC CCGGCNNCCC CCKAKMCNT KGNTGAACMA AAACKCSGGGG      900
GSCNMNMYYY YCNMNGNRIT TNRGGSSNMT TYMAAAMMAN GGGGKYWTYY CKCCNGSCNN      960
GKTYSGGGST TTTCCNTTTS GGGSSATYKG MACCCCKTMT AYCCGGGGGT NTKTKYCCCC      1020
SC                                                                                   1022

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(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

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NNCGNNKNTA TAMAYCWYCT NCACCSGGGA TCWATTGCGG CCGCAATCTT STMAASAGAT      60
CTCKAAATGC GCAMGANCCG CAWCTATTGG KGTGRASCAG ACCAGCGRGA CCTCGCSGKT      120
CKTTYCTTGC AGRGAGGCCK TGGGTGGCRC CGGTGGCAAT GCCAACCGCC CCCCAAAACN      180
CCGCAATMY CRAAAACAA CCGSGGGGTA GKTCCSGGCC GCCAAATMAA TAACCGTKTT      240
AACKCAGGCN ACGGCCAAC GGYCCGCCCC AACCAAGCNA CCTCCCCSCC NATAGGYCCG      300
GTGGGGGGCTG CCKTATYKCC AASTCGTCAY CTCNACGGGM CGGYCCMCWT TCCGCCTCAT      360
CCGTCTCTCC TTMTATTTTC CRTCCACYKG GCGGGGAACY TTTTNYCNC CTTTGS CMAN      420
CACCNAAAGY CNAAAATTNC CMTGCKCKY SNNCAAAAYGR GATTGGGGTY CGKKTPTTNT      480
TCNMCMAAC CCCTNTTNA CGCCCCMATC CCYTWATAAC CCCWMMCMNS ANGKTTGNSA      540
AAKTNNCCCC AAATRCCAAA MTTCTTCGCC NTTTTNTWMCY YYCCTTTCCC CMCCCNWAAA      600
GGSCCRCCYY TCGGGAANTY TCCCNCAAA AWTCAWCCCM TTTCCCNCCA AGAAWTTCG      660

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10081043-022502

SACTCCTTIN TTCNCGGNAM ATANATYYTT YCKTNGGGSK TTCCGMTNCN AMMAATNTCC 720
 RGGGKAAMCC AGKNTNNTCC YYYCCCCCAA NNTYCCYKGG RMCYNNYYCY TTAAANRASR 780
 SAACCKSGG GKCYNCNCSS TARCCCCCAM KAAAATTTCC CCCSKTTTC TYNNKMKRW 840
 GCCCCCSAAM ACTMTWYATT TCCCKCGNNN TTTSYCKKCS KCAMMMWMTG KKNCTTTTTT 900
 YCSCMATAMA CTITNGGKCTC NTCNYGSGCG CMAAANAAGG CGCGSTTCTN TTCWMAMACA 960
 YNTSGNMMMA SAAKAKWATA AWWNTRKKYK TKNNCCCNCC CKCKCTTSEN TNKCCMCKSKS 1020
 GGKGNWKKR GWCTCCWCNC CKCCCNCKNK CCKWATMCCC CCCCCKCGGN NCMNMTTTKT 1080
 CCC 1083

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1069 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GGGGNNKYAT MCAYCWTCTS YACSGGGMNC TATTGCGGCC GCAWYNGTGM GASAGATCTC 60
 GAAYTCGGCA MGA AAAAGW GATGTGCTGG ACCTTMC CGC GCGGGACGCR ACCRACAAAG 120
 RAASCGCGCC ANAATATTGG CCACAKTTGG TCACATATTT ACCCAATTMT AYCAGGAYT 180
 MCCATTCKKG GGACCRACCG CACAATCCCR ATSKTGGTTT GCRAACCTTR ACOGTCCCCA 240
 MYTYCGCCRA STTGAACAGG GGCRAAAAAA CGGCCRAAWY CTCGCCCTGA NTCCCGCTCS 300
 GCGCNAATAA CTAGGCCCAT TKAACGGAAC CGGNGGCCSC NANTTGGCCA ACAGGTCTTR 360
 ACAAGGGGGC CCASYYCGG CGGWTCOCW TTYCACNCCC TNKTCTCKTG CCGAATYCGG 420
 WTCRATNYC CCWTGGGGCT TKTCKYCKYK KYCGGTNCCA AWTCTNGGTA TNCTATRGKG 480
 TCCCTTAAT SCANATCTGG GCKYCCATT NCTGGSNTTC NATTTAMMAN SRRCGGTTCT 540
 TTCTWTTCCRA AACCGSNTGG GCCCNMCCA AAAAATGATN ATAATAATGK YGSCTTTCAA 600
 ACCCGCGCCC CCATTCTRW CSGTTCANC CCCNGNGGT TAAGTGGGA ATTTYNAMC 660
 YCNARGCCCT NATTTSGGNA AAAACCCYCYC GGGYCTCAAA CMNYTTTTT GSKSSNTCGG 720
 GCTCRTCTSC CAAAACCCAA ATTNTYNYGG GGYCKTNA A CMCGGYCRC RCCGGAAATT 780
 TTTTGTGTTA AACCCCAACC TTTTCAASCC NTTTYTYT TRCCSSCSMN TNGSSGGGNT 840
 KSSCCNTCY RARKCCNMN GGGGGWYCYN CCCCRMNTT TTTTTTTTT CGTNNMAAM 900
 NGKTCTTCA AASMCCCCC SCCCCNSAA ACCCCCTNAR GTTTTTYCMMA AANNWYNGN 960
 KNCCCCCCC MNAAAAAAY YCSCCGNRN ACSMSNGGGA MCCCCGGSN NTRKTTTTT 1020
 TNCMSGYCC CSRMASYTT TKAAMANR GAMNSMTTY TNNRGNWNK 1069

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

NGNGGGGKWK MATAATCWT TCTTACGSGG GGATCWATTG CGGGCCGCAW TCTNGTMCAA 60
 SAGATCTCGA TYTCGGGCAM NACCACCWC TCCRAAAAAA ACCCRAAWCT CGGSKCTCYC 120
 GARAAGTGTT GCCCGCKTTR AATTTAACAA ATTCACTGTC ANAGTGTAC GSKCTTACWT 180

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YCCCGGCAAA	GGGGCCACAA	CCTGCAGRGA	SCACYCRATG	GKTGYTGKTS	CNCGGGCCGG	240
CCGGKTNAA	GGACCTGCCT	GGGKTGCS	TMCAANAATC	WYCCGCGGGT	YCGCTGGRAT	300
MCNCAGGGT	GTCAAAAAC	CGAAACAGG	CACSCCANCC	NTTTACGGGS	CTTAAANGA	360
AAAAGGGCTG	ATGCCCCAA	GGGGGCCCG	NCCCAACCTT	CCGTTGGTCA	ACACCCCGGT	420
CTCTCKTGCC	RAATCCGRWT	CCRATNYCNC	CWTGGCCTTK	TKYCTYCTY	CGGTACCCAA	480
ATCTGGGTAT	CCCTASTGT	CCCTAAWTT	CCAAATCTGG	GCTGTCCAQT	TSCTGGCNT	540
TCCAAATTTA	CCANCAACGG	TTTCTTNCAT	NCCAAAAACC	GNTKGCKCC	NRACCCRAAA	600
AAATGAATAA	TAATAANNGG	KCNNTTYCNA	ACNCCGCCCC	CCCNATTCCA	TYSGNTTCCA	660
NMNCCCCCAG	NGGKTAGTGG	GGGAAANYC	TCMACCCYCA	ANCCCTWARS	TTTNGGRAAT	720
KAAACCTCYC	YCNCGGTCCW	TYMAAAAAMA	NTTATTTGGN	NGNTTTCGGG	MWNCKRKNST	780
SCCAAAATCC	MAAATANTTT	YTTGGTYCNA	TWAAAAAMCG	YGNCCMNC	GGAAAAWTTT	840
TTNTGKTSTA	ACCCCAAAAC	YTTTTCMNAA	NCSSKTTTTT	CYTTCCCCC	AMNWTGGGYS	900
GGGNATKGYG	SCYTNCTTTA	TKTKYTYMTW	CMGGGGGNN	MKMTCCMCCC	CCMTTTYCY	960
NYWRTTTTTN	KCCCKCTNMR	NNRAANNNGN	YTCSYNANAA	AAGCNCNCCC	SCCKNCCNA	1020
AAAAWCCCN	NNNARAKTNT	TTMKANNRNM	SKCKNKGKY	YCCCCCWC	YMNMAAAAA	1080
AATMYCCNC	RASANMCASM	NMGGGRNRS	CCCCCCTT	NNNMTMTNT	TTTTTCSRA	1140
GAGCKCCSCG	MNNANMKCK	CTTTTTKNC	NNGNNGN	GGNGMNCCK	CCNAGAMWK	1200
CTKSTCCCKS						1210

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

NGSSSNGNNA	TMCATCWYCT	GYACSGGGMT	CWATTGCGGC	CGCAACTNGT	MAASAGATCT	60
CGAAATCGCG	AAKANACACC	ACGCGCGTGT	MTATACACCG	CAAAATGTTCT	GTKTGCCAAA	120
ACCGAGACGC	GCCGGCCCGG	GGGYTCCAAC	GCKTTCACYR	ACCCGCCAGY	TCAGTGTTTA	180
AACCGGTGYT	RAGGGCCGCA	CCCAACWTAA	ACGCTTTAKC	CAAGRAWYTG	GKTGGCCCCG	240
AGCCACCTCG	TGTGGYTGCC	CTCWYCGGTG	GTAGCGCCGG	TTANCGCCGG	TTCGCGGYTC	300
AMCASCSCG	CGGTRATCCC	AKCNWTCGCC	CGGCCMRACC	CACCGGGCAC	TTTGRACGGT	360
GCCCGCAATT	CAAAYCKYCT	GRWTCCTTMC	AAACACACAC	AAGGCCACCM	SCCACCNA	420
ATMGGGRACT	TTAAGGCCCA	GGCAAAACCT	NTRAKNCCT	CCCGGGCRAA	GGTCCSGCAA	480
SCRATCMMAA	AAAACCKNAT	TTCCCCCAGC	AKCAACCCAA	MMCGSTTTGC	TGCTTCGGGA	540
TTCGAAMCCA	ATTMCWGKGT	NCNWGGGAAA	AACASCNCC	NWTAACCMGG	CCCMCGGGCA	600
ATTTCSGRAA	SAACCCCTNY	CCCGGGTTTT	YCTGTCTCMG	GCCCAANACC	CCCGGGAATC	660
AAAAASGGTC	GGNCAAAANG	GCMAAACCCS	SACCCMACTT	WTTCCRCTTN	GGGGGSGCWN	720
CCKNGTTTAA	AWKSCCTCY	CTSCCCAAAY	TCGGKCMMAA	NNGRKTTGGK	TTNGGCNACC	780
NTTTCGGGAK	CCGGGKGKGT	WGKYCTMNMA	CTTTNTTTTT	SCCCYKAAA	NYSCCCCCCC	840
CGGSSCCCCG	CCCGGGGGGA	NNTTTTTAMA	GKTTYCCCTT	CCCCAMAAAA	ANACCCNYC	900
CCSGGSCCT	TTKRWAAMN	KCTSCCCNCG	GNNGGGGCKM	GGKTTATMT	NNNCCSCCCC	960
TCGCGSAAA	AAATAKMTT	SYCCCCCNC	CTCCNCKNR	GKAMSMSGC	TCCYCTCNC	1020
GCNKNTWAAN	ARSNCCKKN	CNCKYCCGS	NSNGKNCWCD	NCCSTSSNCT	NKGKNCNKN	1080
KAAANAAYNC	NGMSSTSSMN	CNCKC				1105

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

NGSNSNKNNN	TAMAYCWYYC	TSCACSNNGA	ACWANTGCGG	CCRMAWCTNS	TMKASAGATC	60
TMGAAYTCGG	CAAGAGCGGG	AAGAGTGTGT	GCATCTGGTC	ANAGTSTMAA	CRCGGTGCCG	120
CSGGTGGKTR	GASCACMCAT	NTGCGGRACAC	CAAAACCKTC	GCGGGYACCC	GGCKTCGCCT	180
GCAAAWYCC	CCAGGCCACC	TCRAACAAYW	YCTYCTGCAA	CGCARGCCGT	TYCGCGGCCG	240
RATCCTGGKT	CASYYGCCCK	TGCGGTGCC	AAGTACTGG	CS CAYCAAAA	CCGCTCCGGG	300
RAACRAACKT	AAWTYTGCCG	AATTTCTNTC	CCCTGCGCCT	TGATAAAATT	NTNAAGCCAC	360
CGCAAMCCCTY	CGGGCKTCTC	CTCKTGCCRA	ATYCGRWTCC	RATAYCGCCA	TGGCCTNKTC	420
KYCTYCKYCS	GTACCCAAAT	CTTGGGTATC	CTATANTKYC	CCWAAANRCA	AWTCTGGGCK	480
KTCCATKTC	TGGSKTCCRA	ATTTAMMACA	NCGGTTTCTT	TCWTACCAAA	AACCSNTGGG	540
CCCCRACCA	AAAAGGATAA	TAATAAGKGT	CWWWCAAAAC	CCGCGCCCCC	RRTTCAAYCG	600
GTCCARCACC	CCANGNGGTN	AGGTNGGAAT	TYTMAACCCC	CAGCCCATAA	SNITNSGNAA	660
AAACCCCN	GGGYMYCAAA	AMMCTTTTTG	GGGMTTCSGS	CCATKGKCC	AAAACCAAAA	720
TMTTTCYCGT	CRWAAAACCC	GGCCCNCCCG	NAAATTTTTT	GKCAACCCCA	AACCTTTMAM	780
CCNNNTTCY	YCCCNACAA	TNGSGGNGKN	NGSSCNTTYT	TWTTTYNNNA	GGGGGRRWC	840
SNCCCNAA	YYCCNAANK	NKCCCGSNMA	AAAGAGANTT	YCMKAAAAAC	CCCCNCNCCC	900
NAAAYACCCC	MAAAKWTTCM	AAASMSCNNG	YCCCCC			936

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1042 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

NNNGNKNNNY	ATMMAYTCWY	YCTSCACCSG	GGNNWCWATT	GCGGCCRMW	KCTTGTMAS	60
AGATCTMNA	YTCGGCACAG	ASSSGCACAG	ASCCGCGCGG	CTATYCMYCC	GYTGCTCATG	120
CTCAACACGC	TCKTCGGCGW	GRATAATGGC	NCGCGCGCGG	CGCCCAACAG	YTCAYTGCT	180
TCGCCAACGC	CATATWTCAA	CAAGGTRATA	AAASCAAAAC	CGCSGCGCCY	GCCTCTGGGC	240
SCGGRAASC	GTGCCAACCC	RAAACNCKTT	GGGCACYCGG	KTSRACTTTA	AASGGTAATC	300
TCKTCCTCT	GGGCTATGGT	CGGCCACAAA	CCTSYTGCGC	WGGGTCTGGC	CCTGGGYCAC	360
CGYCRNTTT	TAINTNTCK	YCTACACNCT	TKGGTYCAAC	CAACCCACTT	CACMAAATIG	420
TTTTGGGKTR	GGGSGCCGCG	YGTGNNCCGK	TAATAATCSG	NTGKTCSGCC	MYCACCGGWA	480
CCATANCCTG	GCGGGSCCTG	GCAAAATTCC	SAAATCATYT	CCTTCTGRAC	CCCCACAMRC	540
CTNSAAATCC	GRATCAATNC	CCCNKGGCTT	NTCYCTCTCN	GTRCCCAATY	TGGTTTCTAT	600
RKTNCCCYAA	TSCAATTGGS	TTYCRRTSC	YGSTTCCAAN	TTNACAAMAS	GGTTTYTCMT	660
ACCAAAAACC	NTGSSCCNNA	CMNAAAANKNA	RAAAANAKGG	KCTTTYAAAC	CCCCCCTAT	720
TCAWYCGGTN	CMRNWCCCG	NGKAAGGKGN	GAAAYTTHRA	CCCAANCCMT	ARSTTSGNAK	780
AAACCCYCG	GGGTSMCAAA	MKNTWTSSC	CTTCGGMCTT	YCCAAATMSA	AAATYTTCKK	840
KRMNAAAAMC	YGNCCCSAA	ANATTTTGT	NAAMCCCKMA	YYTRTTWMCC	WTTTTCYCC	900
CCMCNNSNSG	GNTNCCCTTY	TYATTTCYMM	MCRNNSGACN	CCCCMNTYTT	TWTTCKWCN	960
MMARGSNNTY	RGRMMNMNCC	CCNCCCNNAK	MTCCNCAAAK	NTTTNAACNN	NNKYCKCCCC	1020
CCCMWNNKNC	CCCMNCMCTT	TM				1042

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

NNSGSGMKKK ATAMATCWCT CTSYACCSNG GMITCWATTGC GGCCGMAWTC TNGTMAASAG 60
 ATCTCGAAAYT CGGCAAAANAK ACGCMAYGTC AAGTGTTRAYY CGGTACACATA TCMTCCGGNG 120
 TCAACMCCAA AGCCGNGTCA CCGYCTCCCT GGGCGCCAC CCCCATCGGT RATGCAACYT 180
 CGCGCGCCAC CGYCAAAAGG KTCWTTTRAGG CGCTAAAGGT CAMCAATTCC TRAGGTMYCN 240
 CACCGTINTT TGGCCCGCCC RAWTYCTRAC CCGCAATWTC GGTAATCGGR AATTGGGGCW 300
 YCGGCTTGGG CAATAAGKTN TTGGGCAACG GCGGRWTCYC NCTGGCCGRA ATTCGCCNAT 360
 TCCKTTAAGC GKTGRACCGT TTYCCCGGYT GCCGTAAYTG YTYCNTGGGC GCCYTCGGCC 420
 CRNAGCASY Y CRCTAACGGY CMCCAGSCAA TACCKTTGGC TTTRAACCA CCGRATNAAY 480
 TGKTACCAC YTCASSGTS CTGRANTTRK TNCNTGRAA AANMCCACCN AACCCGGNTT 540
 RATCTGCTTC MTCANCWTTT SCCGGGTTCT GCGGTTTTGR AAYCTTNATC CMTYCAAAAG 600
 GTTTAMTTTC CCAANRAATT CGGYTTGCCA CCTTGGCCGS GGCTGGTTTM CGMWCCITRR 660
 AMATCCNCCS GCGGSSAAN AMTTSGGNTT SGSCCGGTCC CCCGNAATAT YCNTGGNCT 720
 GNAATTTGSS GGGATCCCN GSGNAYCCGG CWTGKGGGK TNCCCACTGT GWACAATTYC 780
 WKCCGTTCCA AACCCGGGNC GCGGGGGTGG GSCCCTTTT CCTMYNNAAG AAGKGTITGN 840
 NYTTTTCG CNAANPTCA CCSKCNKNT GGNCCNAACY YYCAANTTC CANACCTTTA 900
 AASAAANCYK YGKTYCCCC TTTTMCSSGS SANCCCCCM NMSSKNCGGG AAAAAAGNK 960
 TYNGCCTTAN CNSNKTITT TNKTYCCCC NMWNNSNMCY NCBKCKNRY NGNSNMNCTT 1020
 MKYSKCNNNN SNNNNNCKGN GSNCSGMYK CMNNCNGMYK NGNKSNNCCC MSC 1073

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GNSNGKNKTN TMCAYCWYCT SCACSGGGTC TATTGCGGGC GCAATYNGT CKASAGATCT 60
 CGATYTCGCG AMNANAARTG TCGTCGTCAA TTTCAGKKTG GTCKTCAAYY GGGCCAGGCC 120
 GNGACCRAA CCCTGNGTCA CCAAAANAC CAACAGCWTG AAATWTCAAG GCCRAGGCS 180
 TRTCAATYCC CRASAKTTA ACCGKTCCW TCRAAGGTGC CRAACCAAGC ACCCAGYTCW 240
 CCGCCSGGCA AWTGCGGCTG CCGGCGGNTN TCAGCCTGAT TYCTGACCTC RWTCTGTS 300
 TGGYCAMCNT GGTGAAGGCC CWWCCGCNA AGAACTGGAG GGCRAATTCC CAGGANCCNA 360
 GRAACCCNAG GAACCCGCGG TAKAANCCGG CRAAACCRAG GCGGYTGGCN ATTCCNATTA 420
 NAMSGGTTTG CRACTNGGCC RAACCGITTY CTGGTGGC CTCGGCAACC CTGGACCANT 480
 TACCCCKTM CCGGNMCMAC CYCGGGTNTG TGKYCCCAAT NTGTCYCCGC GNRANTNGGC 540
 CNAATTCCAG GGCNCCANCT TTCCGGCCCN AATTCCTYTG GTTAATCACC GGCNCNCT 600
 GGTTTTGGGC AACCCCNCS CTMTTTTAAA CATTCGSGC CAAATGGGNC STTGGSAAT 660

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TCTNTYCGGT GGGGCSGGCR ANMYTTCTCT YCCCNAAASAN CTTAMYCCAN TTCGSSNTCC 720
 CGGKCAAAWS NGGGGGGGNA AAGGGGCCCC CGGNTSCKCC GGGGKKGGCC CYGGKTTCAC 780
 AANTTTCSGG GKTSTMSCG NVTCSCCCC CSGCCAAGRA CCGNGGTTTT TTTTGAACC 840
 KCMANTCSSA AMCCGCCSSC CCCMAAAGGS GCCTNAAWGR RAYTTNKSCC CNNAACCSGG 900
 CCCCCAKTYS GGGKTTTCNN CNCCSGKKGT CCMSTTTMM MRCCCTTGN GNKTTTTTAN 960
 MGSCCTTHNC CACCCCVCK GGGKCSMNNA GAAKTMWKC CNNGGGNNAN RSCCCCCNN 1020
 GSGKGGGGK MGAGYSCKT CTGCGCN CN YKNTTCCCC C 1061

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GNNGNNKNW ATMCAVCWY CTSCACCSGG GMTCWATTGC GGCCGCAWKY TNGTMAASAG 60
 ATCTMGAAAT CGGCACANAG CGGCACAGAG TGTGTGCATC TGTGTGCANAG CTGTCAACGC 120
 GGTGCCGCSG GTGSTRASCA CMCAITGCGR AACACCAAAC CCGTCCGCGG GYCACC GGCK 180
 TCGCCTGCAA AAYCCTCCAG GCCACCYCRA AACAAWYCT CCTGCAACSC ARSCCGTTC 240
 GCGGCCGRAT CTGGKYCAS YTCGCCGTGC GGTGCGCCAA GGTACTGGCS CWYCRANACC 300
 GCTYCGGGRA ACCNAACGTA AATCTTGCCN AATTGTGNTT CCCCTSCCC TTRATNAATT 360
 TGTAAACCA CGCAAACTY CGGGCKTCTC CTCTGCCRA WTCGRWTC RATNYCGCA 420
 TGGCCTNKTC KYCTYCKYCS GTMCCCAAAT CTGGTATCC TATATTGTCC CTAATGCAA 480
 ATCTGGCTG TCCAITNGT GCGCTTCAA TWAMANCAG NGGTTTCTTY CTCCNAAAC 540
 CCSTTGGCCC CAAACNAAA AATGATNATA ATAATGTGC TNTCAAACCC CGNCCCATY 600
 CNATCSGKCC AMMCCCRGN GGKTANKKG GNAATCTMM AACCCCAAGC CATAASNTTG 660
 SGANAACCY NGNCMGGYCA CCAAAACANY NTNTTGGNY SSNTTGGMN YCATGGCTNN 720
 CMAAAACCA AATACTNYG GYCCAAATA AMMMSGGYC SAMCCGAAA WTTTTYTTGN 780
 KYNAACCA AAKCCTTTTT CNAACCCDAN WNTYCTNCC RCRCMANTGG CNSGGARTKT 840
 SSSCTTNCCA ATGKYCMAA AGNNGGRANA CCARCCCAA TTCCTNNNTN KNKNCNCNST 900
 TRNAAAAGGG GKNTYCNMAA AASCNCNCN CNCTCCCAA AAKAMCCCN AAGAKNTCN 960
 NAANASKYSN NNNSCCCCC CCMNN 986

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

NGNGGGNKRN ATMMAYCWCT SATYYACCSN GGMNMWATTG CGGCCRMWAT CTNGTMKASA 60
 GATCTMGAAA YTCGGCAAG AGYATKCTCG GGGGCCAGAT TTNTGGCCCG CAACCCGGCC 120
 ACTTTGCAWY TCAACAKTCC SGGTGCCCCA AAAAAWTCW ACCCCCATMC TYCKTGCASM 180
 ASYTGCGCCC RATTRAACAC CGGCGCGCW TGCTGCGCCA GGTATTYCAS CAGYTCAAAY 240
 YCTTTKTAGK TAAATCCAG CSGCGCGCCA CNAAGCCGG CGGTKTAGGT GCCTYCRTCA 300

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ATMACCAGCY	CGCCCAGGGY	CACCTTGCCC	AAAACTCCT	GGGTACAGCA	AATTTCGCS	360
CCGGCCAACM	ACCANCOCGA	TYCTGGCNC	AATCYCACCG	GGCCCCGGTGY	TAAAMMAMMA	420
GRATCTCKTC	MANCCCCCAN	TCAGCSYINA	CNGCMACAGC	CCGCCTTCTT	CAMACCGCCA	480
RTACCGGGWT	CAACCGGCCS	GTCAAACCTCA	ACAGGCGGNC	AGGCCTCCCC	CGGANSAAAG	540
GTCTTACSCC	NNYAANAATA	MAAGNTCTGT	TTTCCCCCTC	CASAAANAAA	AANCCCCSGC	600
CGGGCCTTNC	NMMGGGTTTG	GGGMANANAA	AARCNCCGNG	GGAAACGNATC	CGAAMCTTCC	660
CAAGTCNCMT	TWAAACYCN	NNAACCCCC	ANTTTTGGGA	AAGNTCCCC	NTTMYCCCCC	720
TTTTAGSKTS	GGGMYCYCT	TAAAAAAT	CCCCAAAAAG	CCCCGGGAAG	GGTCAMACTG	780
GGNAATTTTC	CAAMCCNWGK	TTNTTYNGGT	TMCGGGGGRA	AATTTCNCTC	CCYNNNGGG	840
CSSGSNNNAT	TAYGGSMNT	TTTNAAWTM	NSGKKTSAAM	YNNKCCMNNN	SNMMSMANNK	900
TNAMCKCCCN	CCTCNGNGKY	CSYNNCCSG	GNAGNGGGRAS	MKCCNANMAA	AYASGNTTNK	960
CGGAAMMWRN	AATKGNNSC	CCGGASMCN	NNNMAAATMT	CNCNKGNSNN	AANRGMRCAN	1020
CCCSNSNGMN	RRGAARMTNY	YCCCCGSKM	GKGNKAAAW	GKYCCCCCM	AAAG	1074

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

NGNGNCKNT	MTACATCWT	CTGCACCSGG	GNTCWANTGC	GGCGCAWY	TGTGCGASAG	60
ATCTCGAAYT	CGGCAMGAGG	ACWCTCGCRA	CGCCCCACA	NACTCTGGCG	TGTGTACCCC	120
ATTGNGCGCK	TCACGCGCCC	AYTGANCCAK	TNACTTGGG	TGCGTYCGC	CKTGCGCGGC	180
GGCCTCACGG	CKCTSCWTCT	RAAGGCWTGG	CGCACCGCAT	TCGGTTTTCT	RAACGCTGGG	240
AAAWTGGCCA	CCGCTGTGCT	TCATGGGNTC	TACGCAACGC	CNGCCCCCAA	CRCTTTCTTA	300
AATCCBGYCC	NTCCTGANCS	CTTTGAAYCC	CGGGGSAAGA	ACTGGTTGCS	CNCGAYCTGC	360
TCGAACCTTRK	TCNAAATCCC	CGANAKTGTT	TCNTAMGYCC	CNCGGAAGG	NGAACCTACT	420
TTCCNGWANG	TCGGCNKCCG	CGCCTTATCA	STCCTGATCA	ACGGGGAAC	GGYKNNSTTG	480
KGGGAAAAAG	RRCTCAATG	MTYGGTCKC	GCTGCGKANC	CGCSCTCTGC	GYCGCNAATG	540
GAAGGCSMAG	GGTTAANGCC	MTTYCNVCCR	RSCCGTSTGA	SGKWTTYCGG	MGGANKAMNN	600
NNKMAWMTTK	TCRNGGCCW	ATSTSCCGG	CKSTTAKAGA	ANACTYCKKW	WCCGNTINTYSC	660
SAAAGNTKCS	CGCMGTTTT	SCKMGMANGN	YCTGATTSA	GGGGGKYKCC	CCCGGGGYTC	720
CGAAAWKRWY	CCYAGGGGGM	GNVCSAGCS	CGMNNATNAG	AGNAAGGKTT	RYGSTSKNCC	780
TYTNKGAGCC	WSCNNCWSAK	ANAAACNNKTT	TGSCSCNTMS	AGNKTNKGR	YCNKNTSTTC	840
TAAGAGGAGC	TATKMKCGCC	CKTGGANGMM	GAGWGMCGC	KYCCCSNKRT	TCNTNGWAAA	900
TATKSAGMGG	TKCCGMAGMK	CCSCGTTKT	TKTGANAAMN	MSMRKNKKTG	CGMGYTCSTC	960
GGGNTTTTGA	GAGTAKTCGS	CSCSSMWGAC	WCSGCMCMNG	AGKNKTNTS	YANTGARGCY	1020
MNNSKTMKMT	MSCSCGCGNA	GGAGNGCCCC	CSANGMSTGY	NKGGNMSSNG	ARAKGATGGS	1080
GGCCNCGMNN	MGMGGANMGA	SNANMGGMGR	GGGGKTKGK	TKCSCCGNS	CSANGRAGAA	1140
GKTCNGSGCN	CGMGKYGKT	KTKTKNTGTG	YSTCMSSMM	NAGAAAAGAG	AGGGC	1195

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10084843.022502

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

CCATCTGATC	GTTGGCAACC	AGCATCGCAG	TGGGAACGAT	GCCCTCATTG	AGCATTTGCA	60
TGGTTTGTG	AAACACGGAC	ATGGCACTCC	AGTCGCCCTT	CCGTTCCCGT	ATCGGCTGAA	120
TTTGATTGGC	AGTGAGATAT	TTATGCCAGC	CGCCAGACAG	CAGACGCGCC	GAGACAGAAC	180
TTAATGGCGC	CGCTAACAGC	GCATTTTGCT	GGTGACCCAA	TGCGACCAGA	TGCTCCACGC	240
CCAGTCGCGT	ACCGTCTTCA	TGGGAGAAAA	TAATACTGTT	GATGGGTGTC	TGGTCAGAGA	300
CATCAAGAAA	TAACGCCGGA	ACATTAGTGC	AGGCAGCTTC	CACAGCAATG	GCATCCTGCT	360
CATCCAGCGG	ATAGTTAATG	ATCAGCCCAAC	TGACGCGTTG	CGCGAGAAGA	TTGTGCACCG	420
CCGCTTTACA	GGCTTGCAGC	CCGCTTCGTT	CTACCATCGA	CACCACCACG	CTGGCACCCA	480
GTTGATCGGC	CGGAGATTTA	ATCGCCGCGA	CAATTTCGGA	CGCGCGCTGC	AGGGCCAGAC	540
TGGAGGTGGC	AACGCCAATC	AGCAACGACT	GTTTGCCCGC	CAGTTGTTGT	GCCACGCGGT	600
TGGGAATGTA	ATTCACTGCC	GCCATCGCGC	CTTCACCTTT	TTCGCCGCTT	TTCGCAGAAA	660
CGTGCGCTGC	CTGGTTTACC	ACGCGGGA	CGGTCTGATA	AGAGACACCG	GCATACTCTG	720
GCATCATCTA	TAACGTTTCT	GTTTTCACAT	TCACCACCTT	GAATTGACTC	TCTTCCGGGC	780
GCTATCATGC	CATACCCGGA	AAGGTTTTCG	GCCATTTCGAT	GGTGTCCGGG	ATCTCGACGC	840
TCTCCCTTAT	GCGACTCTTG	CATTAGGAAG	CAGCCCAGTA	GTAAGTTGAG	GCCGTTGAGC	900
ACCGCCCGCG	CAGGGAATGG	TGCATGCAAG	GAGATGGCGC	CCAACTGTCC	CGCGGCCACG	960
GGGCGTGCAC	CCATACCCAC	GCGCAAAACA	GCGCTCATAT	CGCCGAAAGT	CGCAGCCCGA	1020
TCTTCCCATC	CGGTGATGTC	GGCGATATAG	GCGCCAGCAA	CGCAGCTCTG	GGCGCCGGTG	1080
ATGCCCGCCA	CGATGCGTCC	GGCGTAGAGG	ATCGAGATCT	CGATCCCGCG	AAATTATATC	1140
GACTCACTAT	AGGGGAATTT	TGAGCGGATA	ACAATTCCCT	TCTAGAAATA	ATTTTGTTTA	1200
ACTTTAAGAA	GGAGATATAC	ATATGGGGCA	TCATCATCAT	CATCAGTGA	TCGACATCAT	1260
CGGAGACCGC	CCCACTATCT	GGGAACAGCG	GGCGCGGAG	CGCGTCCAGC	GGGCGCGGGA	1320
TAGGCTCGAT	GACATCCGCG	TCGCTCGGGT	CATTGAGCAG	GACATGCGCC	TGGACAGCCG	1380
CGCAAGATCT	ACCTACCGCA	TCAAGCTCGA	AGTGTCGTTT	AAGATGAGCC	CGCGCAACCT	1440
GAGGGGCTCG	AAAGCACCGA	GCGGTTCCGC	TGAACCGGGC	GCGCGCGAGC	GTACTGTCTG	1500
GACTACCCCC	GCGTCTGTCG	CGGTGACGTT	GGCGGAGACC	GGTAGCACGC	TGCTCTACCC	1560
GCTGTTCAAC	CTGTGGGGTC	CGGCCCTTCA	CGAGAGGTAT	CCGAACGTCA	GATCACCCGC	1620
TCAGGGCACCC	GGTTCCTGGT	CCGGGATCGC	CGAGGCCGCC	CGCGGGACGG	TCAACATTGG	1680
GGCCTTCGAC	GCCTATCTGT	CGGAAGGTGA	TATGGCCGCG	CACAAGGGGG	TGATGAACAT	1740
CGCGCTAGCC	ATCTTCGCGT	AGCAGGTCAC	CTACACCTGG	CCCGGAGTGA	CGCAGCACTT	1800
CACAGTCGAC	GGAAAGGTCC	TGGCGGCCAT	GTACCAGGGC	ACCATCAAAA	CTCTGGGACGA	1860
CCCGCAGATC	GTCGCGCTCA	ACCCGGCGGT	GAACCTGCCC	GGCACCGCGC	TAGTTCCGCT	1920
GCACCGCTCC	GACGGGTCCG	GTGACACCTT	CTTGTTTACC	CAGTACTCTG	CCAAGCAAGA	1980
TCCCGAGGGC	TGGGGCAAGT	CGCCCGGCTT	CGGCACCACC	GTGCAGTCCC	CGGCGGTGCC	2040
GGGTGCGCTG	GGTGAGACCG	GCAACGGCGG	CATGTTGACC	GGTTGCGCGT	AGACACCGGG	2100
TCGCGTGGCC	TATATCGGCA	TCAGCTTCCT	CGACCAGGCC	AGTCAACGGG	GACTCGGCGA	2160
GGCCCAACTA	GGCAATAGCT	CTGGCAATTT	CTTGTGTGCC	GACGCGCAAA	CGATTACAGC	2220
CGCGGCGGCT	GGCTTCGCTA	CGAAAAACCC	GGCGAACCCG	CGGATTTCTA	TGATCGACGG	2280
CGCCGCCGCC	GACGGCTACC	CGATCATCAA	CTACAGTATC	GCCATCGCTA	ACAACCGGCA	2340
AAAGGACGCG	GCCACGCGCG	AGACCTTGCA	GGCATTTCGT	CACTGGGCGA	TCACCGACGG	2400
CACAAAGTGC	TCGTTCTCTG	ACCAGGTTCA	TTTCCAGCCG	GTGCCCGCCG	CGGTGGTGA	2460
GTTTCTGAGC	CGGTTATGCG	CGACGATTTT	CAGCGCTGAG	ATGAAGACCG	ATGCGCTGAC	2520
CTCCTCGCAG	GAGGCAGGTA	ATTTTCGAGC	GATCTCCGGC	GACCTGAAAA	CCGAGATCGA	2580
CCAGGTGGAG	TCGACCGGAG	GTTGCTTGCA	GGGCGAGTGG	CGCGGCGCGG	CGGACCGCGC	2640
CGCCACGGCC	CGCGTGTGTC	GCTTCCAAAG	AGCAGCCAAT	AAGCAGAAGC	AGGAATCTGA	2700
CGAGATCTCG	ACGAATATAT	GTCAGGCCGG	CGTCCAAATC	TTCAGGCGCC	ACGAGGAGCA	2760
GCAGCAGGCG	CTGTCTCTCG	AAATGGGCTT	TGGATTCAGC	TTGCGCGTGC	CTGCTGGCTG	2820
GGTGAGTGCT	GACGCCCGCC	ACTTCCGACTA	CGGTTACGCA	CTCTCTCAGCA	AAACACCGCG	2880
GGACCCGACT	TTTCCCGGCA	AGCCCGCGCC	GGTGCGCCAAT	GACACCCGTA	CTGCTGCTCG	2940
CCGGCTAGAC	CAAAAGCTTT	ACGCCAGCGC	CGAAGCCACC	GACTCCAAAG	CCGCGGCCCG	3000
GTTGGGCTCG	GACATGGGTC	AGTTCTATAT	GCCCTACCCG	GGCACCCGGA	TCAACACGGA	3060

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AACCGTCTCG CTYGACGCCA ACGGGGTGTC TGGAAGCGCG TCGTATTACG AAGTCAAGTT 3120
 CAGCGATCCG AGTAAGCCGA ACGGCCAGAT CTGGACGGGC GTAATCGGCT CGCCCCGCGC 3180
 GAACGCACCG GACGCCGGGC CCCCTCAGCG CTGGTTGTG GTATGGCTCG GGACCCGCAA 3240
 CAACCCGGTG GACAAGGGCG CGGCCAAGCG GCTGGCCGAA TCGATCCGGC CTTTGGTCGC 3300
 CCGCCGCGCG GCGCCGGCCG GGAAGTTCG TCCTACCCCG ACGACACCGA CACCGCAGCG 3360
 GACCTTACCG GCCTGAGAAT TCTGCAGATA TCCATCACAC TGGCGGCCGC TCGAGCACCA 3420
 CCACCACAC CACTGAGATC CGGCTGCTAA CAAAGCCCGA AAGGAAGCTG AGTTGGCTCG 3480
 TGCCACCGCT GAGCAATAAC TAGCATAACC CCTTGGGGCC TCTAAACGGG TCTTGAGGGG 3540
 TTTTTCGCTG AAAGGAGGAA CTATATCCGG AT 3572

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Val Gln Phe Gln Ser Gly Gly Asp Asn Ser Pro Ala Val Tyr Xaa Xaa
 1 5 10 15
 Asp Gly Xaa Arg
 20

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Thr Thr Val Pro Xaa Val Thr Glu Ala Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Thr Thr Pro Ser Xaa Val Ala Phe Ala Arg

10084643-022502

1

5

10

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Asp Ala Gly Lys Xaa Ala Gly Xaa Asp Val Xaa Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Thr Xaa Glu Glu Xaa Gln Glu Ser Phe Asn Ser Ala Ala Pro Gly Asn
 1 5 10 15
 Xaa Lys

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

CTAGTTAGTA CTCAGTCGCA GACCGTG

27

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GCAGTGACGA ATTCACCTCG ACTCC

25

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

CATATGGGCC	ATCATCATCA	TCATCAGCTG	ATCGACATCA	TCGGGACCAC	CCCCACATCC	60
TGGGAACACG	CGGCGGCGGA	GGCGGTCCAG	CGGGCGCGGG	ATAGCGTCGA	TGACATCCGC	120
GTCCGTCGGG	TCATTGAGCA	GGACATGGCC	GTGGACAGCG	CCGGCAAGAT	CACCTACCGC	180
ATCAAGCTCG	AAGTGTCTGT	CAAGATGAGG	CCGGCGCAAC	CGAGGGGCTC	GAAACCACCG	240
AGCGGTTCGC	CTGAAACGGG	CGCCGGCGCC	GGTACTGTCT	CGACTACCCC	CGCGTCTGCT	300
CCGGTGACGT	TGGCGAGAGC	CGGTAGCACG	CTGCTCTACC	CGCTGTTCAA	CCTGTGGGGT	360
CCGGCCTTTC	ACGAGAGGTA	TCCGAACGTC	ACGATCACCG	CTCAGGGGAC	CGGTTCTGGT	420
GCCTGGATCG	CGCAGGCCGC	CGCCGGGACG	GTCAACATTG	GGGCCCTCCG	CGCCTATCTG	480
TCGGAAGGTG	ATATGGCCCG	GCACAAGGGG	CTGATGAACA	TCGCGTAGCG	CATCTCCGCT	540
CAGCAGGTCA	ACTACAACCT	GCCCAGAGTG	AGCAGACACC	TCAAGCTGAA	CGGAAGATGC	600
CTGGCGGCCA	TGTACCAAGG	CACCATCAAA	ACCTGGGACG	ACCCGCAGAT	CGCTGCGCTC	660
AACCCCGGCG	TGAACCTGCC	CGGCACCGCG	GTAGTTCCGC	TGCACCGCTC	CGACGGGTCC	720
GGTGACACCT	TCTTGTTCAC	CCAGTACCTG	TCCAAGCAAG	ATCCCAGAGG	CTGGGGCAAG	780
TCGCCCGGCT	TCGGCACCAC	CGTCGACTTC	CCGGCGGTGC	CGGGTGCGCT	GGGTGAGAAC	840
GGCAACGGCG	GCATGTTGAC	CGGTTGCGCC	GAGACACCGG	CGTGCCTGGC	CTATATCGGC	900
ATCAGCTTCC	TCGACCAGGC	CAGTCAACGG	GGACTCGGCG	AGGCCCAACT	AGGCAATAGC	960
TCTGGCAATT	TCTTGTTCGC	CGACGCGCAA	AGCATTACAG	CCGCGGCGCG	TGGCTTCGCA	1020
TCGAAACACC	CGGCGAACCA	GGCGATTTCG	ATGATCGACG	GGCCCGCCCC	GGACGGCTAC	1080
CGGATCATCA	ACTACGAGTA	CGCCATCGTC	AACAACCGCG	AAAAGGACGC	CGCCACCGCG	1140
CAGACCTTGC	AGGCATTTCG	GCATCTGGCG	ATCACCGACG	GCAACAAGGG	CTCGTTCCTC	1200
GACCAAGTTT	ATTTCCAGCC	GCTGCCGCCG	CGCGTGGTGA	AGTTGTCTGA	CGCGTTGATC	1260
GCAGCACTTT	CCAGCGCTGA	GATGAAGACC	GATGCCGCTA	CCCTCGCGCA	GGAGGACAGT	1320
AATTTTCGAG	GGATCTCCGG	CGACCTGAAA	ACCCAGATCG	ACCAGGTGGA	GTGACGCGCA	1380
GGTTGCTTGC	AGGGCCAGTG	GCGCGGCGCG	GCGGGGACGG	CCGCCACGGC	CGCGTGGTGT	1440
CGCTTCCAAG	AAGCAGCCAA	TAAGCAGAAG	CAGGAACCTG	ACGAGATCTC	GACGAATATT	1500
CGTCAGGCCG	CGGTCGAATA	CTCAGAGGCC	GACGAGGAGC	AGCAGCAGGC	GCTGTCTCTG	1560
CAAAATGGCT	TTGTGCCGCT	AACGGCCGCG	TCGCCCGCGT	CGACCGCTCG	AGCGCCACCC	1620
GCACCGGCGA	CACCTGTTGC	CCCCCACCA	CCGCGCGCGC	CCAACACGCC	GAATGCCGAC	1680
CCGGGCGCAT	CCAACGCGAC	ACCTCCGCGG	GCCGACCCGA	ACGCACCGCG	GCCACTGTCT	1740
ATTGCCCCAA	ACGCACCCCA	ACCTGTCCGG	ATGCAACAAC	CGGTTGGAGG	ATTACGCTTC	1800
CGCGTGCCTG	CTGGCTGGGT	GGAGTCTGAC	GCGCCCACTT	TCGACTACGG	TTCAACCACTC	1860
CTCAGCAAAA	CCACCGGGGA	CCCGCCATT	CCCGGACACG	CGCCGCCGGT	GGCCAAATGAC	1920
ACCCGTATCG	TGCTCGCGCG	CTAGACCAA	AAGCTTTACG	CCAGCGCCGA	AGCCACCGAG	1980
TCCAAGGCCG	CGGCCCGGTT	GGGCTCGGAG	ATGGGTGAGT	TCTATATGCC	CTACCCGGGC	2040
ACCCGGATCA	ACCAGSAAAC	CGTCTCGCTC	GACGCCAACG	GGGTGTCTGG	AGCGCGCTCG	2100
TATTACGAAG	TCAAGTTTCAG	CGATCCGAGT	AAGCCGAACG	GCCAGATCTG	GACGGGCGTA	2160

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ATCGGCTCGC	CCGCGCGGAA	CGCACCGGAC	GCCGGGCCCC	CTCAGCGCTG	GTTTGTGGTA	2220
TGGCTCGGGA	CCGCCAACAA	CCGGTGGAC	AAGGGCGCGG	CCAAGGCGCT	GGCCGAATCG	2280
ATCCGGCCTT	TGGTCGCCCC	GCCGCGGCG	CCGGCACCGG	CTCCTGCAGA	GCCGCTCCG	2340
GCGCCGCGC	CGGCCGGGGA	AGTCGTCTCT	ACCCCGACGA	CACCGACACC	GCACGGGACC	2400
TTACCGGCCT	GA					2412

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Met	Gly	His	His	His	His	His	Val	Ile	Asp	Ile	Ile	Gly	Thr	Ser	
1				5				10					15		
Pro	Thr	Ser	Trp	Glu	Gln	Ala	Ala	Ala	Glu	Ala	Val	Gln	Arg	Ala	Arg
			20				25					30			
Asp	Ser	Val	Asp	Asp	Ile	Arg	Val	Ala	Arg	Val	Ile	Glu	Gln	Asp	Met
		35				40					45				
Ala	Val	Asp	Ser	Ala	Gly	Lys	Ile	Thr	Tyr	Arg	Ile	Lys	Leu	Glu	Val
		50				55					60				
Ser	Phe	Lys	Met	Arg	Pro	Ala	Gln	Pro	Arg	Gly	Ser	Lys	Pro	Pro	Ser
				70					75					80	
Gly	Ser	Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro
				85					90					95	
Ala	Ser	Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr
			100				105						110		
Pro	Leu	Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn
			115				120					125			
Val	Thr	Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln
		130				135					140				
Ala	Ala	Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser
				150					155					160	
Glu	Gly	Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala
				165					170					175	
Ile	Ser	Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His
				180				185					190		
Leu	Lys	Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile
			195				200					205			
Lys	Thr	Trp	Asp	Asp	Pro	Gln	Ile	Ala	Ala	Leu	Asn	Pro	Gly	Val	Asn
			210			215					220				
Leu	Pro	Gly	Thr	Ala	Val	Val	Pro	Leu	His	Arg	Ser	Asp	Gly	Ser	Gly
				230						235				240	
Asp	Thr	Phe	Leu	Phe	Thr	Gln	Tyr	Leu	Ser	Lys	Gln	Asp	Pro	Glu	Gly
				245					250					255	
Trp	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Thr	Thr	Val	Asp	Phe	Pro	Ala	Val
				260				265					270		
Pro	Gly	Ala	Leu	Gly	Glu	Asn	Gly	Asn	Gly	Gly	Met	Val	Thr	Gly	Cys
				275			280					285			
Ala	Glu	Thr	Pro	Gly	Cys	Val	Ala	Tyr	Ile	Gly	Ile	Ser	Phe	Leu	Asp

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290 295 300
 Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser
 305 310 315 320
 Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala
 325 330 335
 Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp
 340 345 350
 Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile
 355 360 365
 Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala
 370 375 380
 Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp
 385 390 395 400
 Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp
 405 410 415
 Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala
 420 425 430
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu
 435 440 445
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly
 450 455 460
 Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
 465 470 475 480
 Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser
 485 490 495
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu
 500 505 510
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala
 515 520 525
 Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro
 530 535 540
 Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro
 545 550 555 560
 Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro
 565 570 575
 Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn
 580 585 590
 Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser
 595 600 605
 Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr
 610 615 620
 Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr
 625 630 635 640
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu
 645 650 655
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu
 660 665 670
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser
 675 680 685
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys
 690 695 700
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile
 705 710 715 720
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp
 725 730 735

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Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
 740 745 750
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
 755 760 765
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
 770 775 780
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
 785 790 795 800
 Pro Ala

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GGATCCAAAC CACCGAGCGG TTCGCCTGAA ACGG 34

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

CGCTGCGAAT TCACCTCCGG AGGAAATCGT CGCGATC 37

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

CATATGGGCC ATCATCATCA TCATCACGGA TCCAAACCAC CGAGCGGTTC GCCTGAAACG 50
 GGCGCCGGCG CCGGTACTGT CGCGACTACC CCCGCTCGT CGCCGGTGAC GTTGGCGGAG 120
 ACCGGTAGCA CGCTGCTCTA CCCGCTGTTC AACCTGTGGG GTCCGCGCTT TCACGAGAGG 180
 TATCCGAACG TCACGATCAC CGCTCAGGGC ACCGGTTCTG GTGCCGGGAT CGCGCAGGCC 240

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GCCGCCGGGA CGGTCAACAT TGGGGCCTCC GACGCCTATC TGTCGGAAGG TGATATGGCC 300
 GCGCACAAAGG GGCTGATGAA CATCGCGCTA GCCATCTCCG CTCAGCAGGT CAACTACAAC 360
 CTGCGCCGAGG TGAGCGAGCA CCTCAAGCTG AACGGAAAAG TCCTGCGCGC CATGTACCAG 420
 GGCACCATCA AAACCTGGGA CGACCCGCGAG ATCGCTCGCG TCAACCCCGG CGTGAACCTG 480
 CCGGCGACCG CGGTAGTTCC GCTGCACCGG TCCGACGGGT CCGGTGACAC CTTCTTGTTC 540
 ACCCAGTACC TGTCFAACGA AGATCCCGAG GGCCTGGGGCA AGTCGCGCGG CTTCCGCGAC 600
 ACCGTGCACT TCCCGCGCGT GCCGGGTGCG CTGGGTGAGA ACGGCAACGG CGCGATGTGT 660
 ACCGGTTGCG CCGAGACACC GGGCTGCGTG GCCATATATCG GCATCAGCTT CCTCGACCAG 720
 GCGAGTCAAC GGGGACTCGG CGAGGCCCAA CTAGGCAATA GCTCTGGCAA TTTCTTGTTC 780
 CCGGACGCGC AAAGCATTCA AGCCGCGGCG GCTGGCTTCG CATCGAAAAC CCGCGCGAAC 840
 CAGGCGATT TCGATGATCGA CGGGCCCGCC CCGGACGGCT ACCCGATCAT CAACTACGAG 900
 TAGCCCATCG TCAACAACCG GCAAAAGGAC GCCGCCACCG CGCAGACCTT GCAGGCATT 960
 CTGCACTGGG CGATCAACGA CGGCAACAAG GCCTCGTTCC TCGACCAGGT TCATTTCAG 1020
 CCGCTGCCCG CCGCGGTGGT GAAGTTGTCT GACCGGTTGA TCGCGACGAT TTCTCTCCGA 1080
 GGTGGCAGTG GGGGAGGCTC AGGTGGAGGT TCTGGCGGGA GCGTGCCAC AACCGCCGCG 1140
 TCGCCCGCGT CGACCGCTGC AGCCGCCACC GCACCGCGCA CACCTGTTGC CCCCACCACA 1200
 CCGGCGCGCG CCAACACGCG GAATGCCGAG CCGGGCGATC CCAACGCGAG ACCTCCGCGG 1260
 GCGGACCGCA ACGCACCGCC GCCACCTGTC ATTGCCCAA ACGCACCCCA ACCTGTCCGG 1320
 ATGCACAACC CGGTGAGAG ATTCACTTC GCGCTGCGTT CTGGCTGGAT GAGTCTGAC 1380
 GCGGCCCACT TCGACTACGG TTCAGCACTC CTCAGCAAAG CCACCGGGGA CCGCCATT 1440
 CCGGACGAGC CGCCGCCGCT GGCCAATGAC ACCCGTATCG TGCTCGGCGC GTAGACCAA 1500
 AAGCTTTTAC CCGAGCGCGCA AGCCACCGAG TCCAAAGCGG CGGCCCGGTT GGGCTCGGAG 1560
 ATGGGTGAGT TCTATATGCC CTACCCGGGC ACCCGGATCA ACCAGGAAAC CGTCTCGCTC 1620
 GAGCCCAACG GGGTGTCTGG AAGCGCGTGC TATTACGAAG TCAAGTTTCA CGATCCGAGT 1680
 AAGCCGAACG GCCAGATCTG GACGGGCGTA ATCGGCTCGC CCGCGCGCAA CGCACCGGAG 1740
 GCGGGGCCCC CTCAGCGCTG GTTTGTGGTA TGGCTCGGGA CCGCCAACAA CCGGCTGGAG 1800
 AAGGGCGCGC CCAAGGCGCT GGCGAATCG ATCCGGCCTT TGGTCGCGCC CGCGCGCGCG 1860
 CCGGACCGCG CTCTTGAGA CGCCGCTCCG CGCGCGCGCG GAGCCCGGGA AGTCGCTCCT 1920
 ACCCGCAGCA CACCGACACC GCAGCGGACC TTACCGGCGT GA 1962

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Met Gly His His His His His Gly Ser Lys Pro Pro Ser Gly Ser
 1 5 10 15
 Pro Glu Thr Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 20 25 30
 Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 35 40 45
 Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 50 55 60
 Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 65 70 75 80
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 85 90 95
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser

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100 105 110
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
 115 120 125
 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
 130 135 140
 Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 145 150 155 160
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 165 170 175
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 180 185 190
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 195 200 205
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 210 215 220
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 225 230 235 240
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 245 250 255
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe
 260 265 270
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 275 280 285
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 290 295 300
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 305 310 315 320
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 325 330 335
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 340 345 350
 Ile Ala Thr Ile Ser Ser Gly Gly Gly Ser Gly Gly Ser Gly Gly
 355 360 365
 Gly Ser Gly Gly Ser Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
 370 375 380
 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
 385 390 395 400
 Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
 405 410 415
 Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Val Ile Ala Pro
 420 425 430
 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
 435 440 445
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
 450 455 460
 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
 465 470 475 480
 Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
 485 490 495
 Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
 500 505 510
 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
 515 520 525
 Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
 530 535 540

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Ser	Gly	Ser	Ala	Ser	Tyr	Tyr	Glu	Val	Lys	Phe	Ser	Asp	Pro	Ser	Lys
545					550					555					560
Pro	Asn	Gly	Gln	Ile	Trp	Thr	Gly	Val	Ile	Gly	Ser	Pro	Ala	Ala	Asn
				565					570						575
Ala	Pro	Asp	Ala	Gly	Pro	Pro	Gln	Arg	Trp	Phe	Val	Val	Trp	Leu	Gly
			580					585						590	
Thr	Ala	Asn	Asn	Pro	Val	Asp	Lys	Gly	Ala	Ala	Lys	Ala	Leu	Ala	Glu
		595					600					605			
Ser	Ile	Arg	Pro	Leu	Val	Ala	Pro	Pro	Pro	Ala	Pro	Ala	Pro	Ala	Pro
	610					615					620				
Ala	Glu	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Gly	Glu	Val	Ala	Pro	Thr
625					630					635					640
Pro	Thr	Thr	Pro	Thr	Pro	Gln	Arg	Thr	Leu	Pro	Ala				
				645					650						

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